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RESULT 2
US-10-273-992-1
; Sequence 1, Application US/10273992
; Patent No. 6664093
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: CL001200DIV
; CURRENT APPLICATION NUMBER: US/10/273,992
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3377
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; ORGANISM: Human
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Matches 3377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-09-667-373-3  
Sequence 3, Application US/09667373  
Patent No. 6524840  
GENERAL INFORMATION:  
APPLICANT: Donoho, Gregory  
APPLICANT: Turner, C. Alexander Jr.  
APPLICANT: Neble, Michael C.  
APPLICANT: Friedrich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: No. 6524840el Human Endothelin Converting  
TITLE OF INVENTION: Enzyme-Like Proteins and Polynucleotides Encoding the Same  
FILE REFERENCE: LEX-0043-USA  
CURRENT APPLICATION NUMBER: US/09/667,373  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/156,102  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: US 60/176,689  
PRIOR FILING DATE: 2000-01-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 2652  
TYPE: DNA  
ORGANISM: homo sapiens  
US-09-667-373-3

Query Match 64.3%; Score 2172.6; DB 4; Length 2652;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2175; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 371 GACTATGCTGGAGATTTCAGAAAGGAGACAGACAGCTGTTAGGCTCACGACGACGCTGGA 430  
DB 474 GAGTGGGCTGGAGATTTCAGAAAGGAGACAGACAGCTGTTAGGCTCACGACGACGCTGGA 533  
QY 431 GCTGCTTAGACAGAGTGCCTCTCTACTGCTGCTGACAGCTCTTGTGGGCTGCTTGGG 490  
DB 534 GCTGCTTAGACAGAGTGCCTCTCTACTGCTGCTGACAGCTCTTGTGGGCTGCTTGGG 533  
QY 491 CCTAGGAGGTCAGATACACAGAGACCATCCACAGACCTGCTTACAGAGGCTGCAAT 550  
DB 594 CCTAGGAGGTCAGATACACAGAGACCATCCACAGACCTGCTTACAGAGGCTGCAAT 653  
QY 551 TCGAGTGGCTGGAATAATCTGAGATCCCTGACCGAGGGGTAGCCCTCTGTAGAGATT 610  
DB 654 TCGAGTGGCTGGAATAATCTGAGATCCCTGACCGAGGGGTAGCCCTCTGTAGAGATT 713  
QY 611 TTACAGATTCTCTGAGGGGCTGAGATTGAGAGAAACCCCTGCTCCGATGGGCTTCTGG 670  
DB 714 TTACAGATTCTCTGAGGGGCTGAGATTGAGAGAAACCCCTGCTCCGATGGGCTTCTGG 773  
QY 671 CTGGAACACCTTCAACAGCCTCTGGAGCCAAAACAGAGGCTATCTGAAGACCTGCTTGA 730  
DB 774 CTGGAACACCTTCAACAGCCTCTGGAGCCAAAACAGAGGCTATCTGAAGACCTGCTTGA 833

QY 731 AAACACACCTTCAACCTCCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790  
DB 834 AAACACACCTTCAACCTCCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 893  
QY 791 TTGCTTACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850  
DB 894 TTGCTTACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953  
QY 851 GAAAGATTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910  
DB 954 GAAAGATTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013  
QY 911 GAAAGATTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970  
DB 1014 GAAAGATTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073  
QY 971 CTCTAAGATTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030  
DB 1074 CTCTAAGATTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133  
QY 1031 TCGGATTAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1090  
DB 1134 TCGGATTAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1193  
QY 1091 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150  
DB 1194 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1253  
QY 1151 GCAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1210  
DB 1254 GCAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1313  
QY 1211 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1270  
DB 1314 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1373  
QY 1271 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1330  
DB 1374 CATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1433  
QY 1331 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1390  
DB 1434 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1493  
QY 1391 GGAACCAACATCTGAGCAATTAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1450  
DB 1494 GGAACCAACATCTGAGCAATTAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1553  
QY 1451 CCTGAGCCAGAGCTTGTAGTCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1510  
DB 1554 CCTGAGCCAGAGCTTGTAGTCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613  
QY 1511 GAAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1570  
DB 1614 GAAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1673  
QY 1571 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1630  
DB 1674 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1733  
QY 1631 GGGAGATGATCAAGAGAAATCCGAGACCGCATTTAGAGAGAGAGAGAGAGAGAGAG 1690  
DB 1734 GGGAGATGATCAAGAGAAATCCGAGACCGCATTTAGAGAGAGAGAGAGAGAGAGAG 1793  
QY 1691 GGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1750  
DB 1794 GGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1853  
QY 1751 TTTCCAGACTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1810  
DB 1854 TTTCCAGACTTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913



Db 962 CGAGATTACTACCTAAACAGACCGCCATGAGAAAGTGTACTGCTACTGCTGATAC 1021  
Qy 1092 ATGAGAGAACTGGGAGATGCTGTGGGTGGGCGGCCCTCTCCAGAGGAGAGATGACAG 1151  
Db 1022 ATGAGAGAGCTGGGAGATGCTGTGGGTGGGCGGCCCTCTCCAGAGGAGAGATGACAG 1081  
Qy 1152 CAGGTCTGAGATGAGATACAGCTGGCCAACTCACTGCCCCAGAGCCAGGCGCG 1211  
Db 1082 CAGGTCTGAGATGAGATACAGCTGGCCAACTCACTGCCCCAGAGCCAGGCGCG 1141  
Qy 1212 GACGAGAGAAAGATCTACCAAGATGAGCATTTGGAGCTGAGGCTCTGGCGCCCTCC 1271  
Db 1142 GATGAGAGAAAGATCTACCAAGATGAGCATTTGGAGCTGAGGCTCTGGCGCCCTCC 1201  
Qy 1272 ATGAGATGCTGTAGATTCCTGTCTTCTTCTGTCTGATGAGATGAGATGAGATGAG 1331  
Db 1202 ATGAGATGCTGTAGATTCCTGTCTTCTTCTGTCTGATGAGATGAGATGAGATGAG 1261  
Qy 1332 CCTGTGGTGGTGTATGAGATGAGATTTATTTGACGAGGTCTGAGCTCATCAACCGCAG 1391  
Db 1262 CCTGTGGTGGTGTATGAGATGAGATTTATTTGACGAGGTCTGAGCTCATCAACCGCAG 1321  
Qy 1392 GAAACAAGATCTGAAACAATTACTGATCTGAAACCTGTGCAAAAGAACCTCAAGC 1451  
Db 1322 GAGCCAAAGTCTCTGAAACAATTACTGATCTGAAACCTGTGCAAAAGAACCTCAAGC 1381  
Qy 1452 CTGGAACGAGCTTTGAGTGTGCAAGAGAGAGCTGTGAGAGCCCTCTATGAGCACTAG 1511  
Db 1382 CTGGAACGAGCTTTGAGTGTGCAAGAGAGAGCTGTGAGAGCCCTCTATGAGCACTAG 1441  
Qy 1512 AAGTCTGTGTGCGAGAGTGGAGAGCTGTGATCTCCAAACGAGATGAGCGCCCTTGGCTT 1571  
Db 1442 AAGTCTGTGTGCGAGAGTGGAGAGCTGTGATCTCCAAACGAGATGAGCGCCCTTGGCTT 1501  
Qy 1572 GCTTTGGGCTGCTCTTGTGAGAGCGCACTTTGACCGGCAAAAGAAATTTGACAG 1631  
Db 1502 GCTTTGGGCTGCTCTTGTGAGAGCGCACTTTGACCGGCAAAAGAAATTTGACAG 1561  
Qy 1632 GGGATATGAGCGAAATTCGGGACCGCATTTGAGAGAGCCCTGGGACAGCTGTGAGATG 1691  
Db 1562 GGGATATGAGCGAAATTCGGGACCGCATTTGAGAGAGCCCTGGGACAGCTGTGAGATG 1621  
Qy 1692 GATGAGAGAGCCCGGAGGAGGAGGAGAGAGAGAGATGCACTATGATGATGATGATG 1751  
Db 1622 GATGAGAGAGCCCGGAGGAGGAGGAGGAGAGAGAGATGCACTATGATGATGATGATG 1681  
Qy 1752 TTCCGAGACTTATCTGTGAGGCGCAAGAGCTGATGATGATGATGATGATGATGATG 1811  
Db 1682 TTCCGAGACTTATCTGTGAGGCGCAAGAGCTGATGATGATGATGATGATGATGATG 1741  
Qy 1812 TCTGAGATTTCTTTTCCAAACATGTTGATTTTGTACAACTTCTGTGCAAGTTATG 1871  
Db 1742 TCTGAGATTTCTTTTCCAAACATGTTGATTTTGTACAACTTCTGTGCAAGTTATG 1801  
Qy 1872 GGTGACAGCTCCGCAAGCTCCGAGCGGAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 1931  
Db 1802 GGTGACAGCTCCGCAAGCTCCGAGCGGAGACAGTGAAGTGAAGTGAAGTGAAGTGAAG 1861  
Qy 1932 AATGCTACTACCTTCCAACTGAAATGAGATGCTTCCCGCTGGATCTCTGAGGCGC 1991  
Db 1862 AATGCTACTACCTTCCAACTGAAATGAGATGCTTCCCGCTGGATCTCTGAGGCGC 1921  
Qy 1992 CCGTTTCTAGCCCGCAACCCCAAGGCGCTGAACTTGGTGGCATCGGTGTGATGATG 2051  
Db 1922 CCGTTTCTAGCCCGCAACCCCAAGGCGCTGAACTTGGTGGCATCGGTGTGATGATG 1981  
Qy 2052 GGGCATGATGATGAGATGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 2111  
Db 1982 GGGCATGATGATGAGATGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 2041  
Qy 2112 CTGCGGCGCTGTGAGAGATGAGTCCCTGGAGCCTTTCGGAACCAACGAGCTGATG 2171  
Db 2042 CTGCGGCGCTGTGAGAGATGAGTCCCTGGAGCCTTTCGGAACCAACGAGCTGATG 2101  
Qy 2172 GAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2231  
Db 2102 GAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2161  
Qy 2232 GGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2291  
Db 2162 GGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2221  
Qy 2292 CTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2351  
Db 2222 CTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2281  
Qy 2352 TTCTGTGGGATTTTCCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2411  
Db 2282 TTCTGTGGGATTTTCCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2341  
Qy 2412 GGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2471  
Db 2342 GGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2401  
Qy 2472 TTCCGTGATCTCTGCGGAGCTTGGGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2531  
Db 2402 TTCCGTGATCTCTGCGGAGCTTGGGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2461  
Qy 2532 CTGTGTGAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2588  
Db 2462 CTGTGTGAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2521  
Qy 2588 TGGGAGAGCTCTCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2648  
Db 2522 TGGGAGAGCTCTCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2581  
Qy 2648 GGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2705  
Db 2582 GGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2641  
Qy 2706 ACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2765  
Db 2642 ACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2701  
Qy 2766 TGTGATCATCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2824  
Db 2702 TGTGATCATCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2758  
Qy 2825 ATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2884  
Db 2759 ATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2818  
Qy 2885 GCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2944  
Db 2819 GCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2873  
Qy 2945 -AGGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3003  
Db 2874 -AGGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2933  
Qy 3004 CTACCCCACTCACCTGTGCTCTTGTGCACTGCTCTCCAGTGTGCTGTGATCTTTC 3063  
Db 2934 CTACCCCACTCACCTGTGCTCTTGTGCACTGCTCTCCAGTGTGCTGTGATCTTTC 2989  
Qy 3064 ACTGAC-----AGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 3108  
Db 2990 ACTGAC-----AGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 3049  
Qy 3109 GCT--GCCCATGTTTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3166  
Db 3050 GCT--GCCCATGTTTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3109  
Qy 3167 TCTGTGTCTTGAAGG-ACAAGCTTGAAGATGATGATGATGATGATGATGATGATGATG 3225  
Db 3110 TCTGTGTGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3169













[illegible]

## RESULT 9

US-08-646-273-24  
: Sequence 24, Application US/08646273  
: Patent No. 606502  
: GENERAL INFORMATION:  
: APPLICANT: Kroegeer, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,  
: APPLICANT: Martin, Jacob, Elard, Olier, Rainer, Sudkowski, Thomas, Hille, Heinz  
: TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
: NUMBER OF SEQUENCES: 36  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Keil & Weinkauff  
: STREET: 1101 Connecticut Avenue  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: USA  
: ZIP: 20036  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
: COMPUTER: IBM AT-compatible, 80486 processor  
: OPERATING SYSTEM: MS-DOS version 6.0  
: SOFTWARE: Wordperfect version 5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/646,273  
: FILING DATE: 16-NOV-1994  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: PCT/EP94/03706  
: FILING DATE: 11-NOV-1994  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 2533 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: CDNA for mRNA  
US-08-646-273-24

Query Match	29.7%	Score 1003.6;	DB 3;	Length 2533;
Best Local Similarity	68.4%	Pred. No. 4.9e-230;		
Matches 1435; Conservative	0;	Mismatches 654;	Indels 9;	Gaps 3;

QY	454	TACTGCTGGCTGCACTGCTTTCGCGCTCCCTCTGTGGCCCTGAGGGTCCAGATCCAGAG	513
Db	20	TACTTCTGCGCGAGACTGGGTGGCTCTTGGGAGCACTGGGATCCAGATCCAGACA	78
QY	514	AACCATCCCAAGACACTGCTCTTACAGAGGCGCTGCATTCGATGGCTGGAATAATCCCTGG	573
Db	79	--AGATCCCCCTCTGTGTGCTCTGAGCGAAGCTTGTCTCAATGACCAAGCTCCATCTTGA	136
QY	574	AGTCCCTGAGCCGAGGGGTGAGCCCTGTGTAGAGACTTTCACAGTCTCTGTGTGGGGCT	633
Db	137	GCTCATGAGACCCCAAGTGGACCCCTGCTCATGACTTCTTGAGCTAACCCGTGTGGGGCT	196
QY	634	GGATTCCGAGGAACCCCTGCTGCCATGGGCGTCTCTGCTGGAAACCTTCAACAGCTCT	693
Db	197	GGATCCAGGGCCAAACCAAGTCCCTGATGAGCACTACCGTGGGGAGCTTTCAGCAACCTCT	256
QY	694	GGGACCAAAACAGGCGCATCTACTGAAAGCACTGCTTGAATAACCAACCACTTCACTCCAGCA	753
Db	257	GGGAACACACCAAGCAATCATCAGACCTCTCTGAAACTTCCACGGCCCAAGCTGAGC	315
QY	754	GTGAAGCTGAGCAGAAAGCACAGCGCTTCTAATCTTGTGCTACAGGTGAGCGCATTTG	813
Db	316	--GAGGAGAGAGAAAGGCGAGATATCTACCGGTGCTGATGAAAGACAGATCG	373
QY	814	AGAGCTGGAGCCCGACCACTGAGAGACTCATTTGAGAAATTTGTGTGGAACTTA	873
Db	374	AGGAGCTCAGGGCCCAACCTCTAATGTGAGTTGATTGAAAGGCTCGGGGGCTGGAACTACA	433
QY	874	CGGGGCGCTGGGACACAGACAACTTTATGAGAGGTGTGAAGGAGTACAGGACCTACA	933
Db	434	CAGGCTCCCTGGGACCAAGACAACTTCCAGAGACCTGTGAGGTGTACACCGCCCATACC	493
QY	934	GGGGCAACCCATTCTTCAACCGTCTACATCAGTGGCGACTCTAAGAGTTCCAAACAGCAATG	993
Db	494	GAOCTCAACCTTCTTCTCTGTCTATGTCAATGCGGATTCAGAAACTCCAAACGACAG	553
QY	994	TTATTCAGGTGACCAAGTCTGGGCTCTTTCTGGCCTCTCGGAGTTACTATTAAACAGAA	1055
Db	554	TGATTCAGGTGACCAAGTCTGGGCTTGGCCTCCAGAGACCTAATTAACCTGAACAAA	613
QY	1054	CTGCCAATGAAAGTGTCTCATCTGCTCATCTGAAATTCATGGAAGAACTGGGGAGTCTGC	1113
Db	614	CTGAAACGAAAGGTGTCTGACCGGATATCTGAATCAATATGTCTCAAGCTGGGAGAGCTGC	673
QY	1114	TGGGTGGGCGGCC---ACCTCCACGAGGAGAGAGATGACACAGGTGTGAGTTGAGA	1170
Db	674	TGGGCGGGGGGAGAGAGAGGCAATCGGCCCCAGATGACAGATCTTGAACCTTTGAGA	733
QY	1171	TACAGCTGGCCAAATCAAGTGTCCCGAGACAGCGCGCGGACGAGAGAGAAATCTAAC	1230
Db	734	CGGCACTGGCCAAATCAATCACTATCCACAGGAGAAAGCGCGATGAGGAGCTCATCTAC	793
QY	1231	ACAAAGTATGAGATTTGGAGTGTGACAGGCTCTGGGGCTCTCAATGATCTGTGAGTTCC	1290
Db	794	ACAAAGTATGAGCGGACGAGCTGACAGACTTGGGACCCGACCATCAACGTGTGGCTTTTC	853
QY	1291	TGTCTTCTTGTCTGTCACTTGGAGTTGATGACTCTGAGCTGTGTGGTGTGTATGGA	1350
Db	854	TCAACACCATTTTCTACCCCGTGGAGATCAATGATTCGAGCTTATTTGTCTATGACA	913
QY	1351	TGGAATTTTGGACAGGTGTCAAGTCTATCAACCGGACGGAAACCAAGCATCTTGAA	1410
Db	914	AGGAATACCTTGAAGAGATCTCACTCATCAACACACCGAGAGATGCTGTCTCAAC	973
QY	1411	ATTACCTGATTTGGAACCTGTGTGAAAAAGACACTTCAAGCTGTGACCGAGCTTTGAGT	1470
Db	974	ACTACATGATCTGAACTGTGTGGAAAAACAACTCTTCTTTGACACAGGCTTTGAG	1033
QY	1471	CTGACAAAGAGACCTGTGGAGACCTCTATATGCACTAAGAAATCTCTGTGCGGAGT	1530
Db	1034	ACGCGGATGAGAAATTTATGGAATCATGTCGAGGACCAAGAGACCTGTCTTCTTGCT	1093
QY	1531	GGGAGACCTGATCTCAACACGAGTACGCCCTTGGCTTGTGGGGTCCCTCTTGC	1590

Db	1094	GGAGCTTTGGGTGAGTCAACAGAAAACAACCTGGCTTTGGCTGGGGCCCACTGTTTG	1153
OY	1591	TGAAGGCCACGTTTGAACCGGCAAAGCAAGAAATTGCAGAGGGATGATCAAGCAATCC	1650
Db	1154	TCAAAAGCAACCTTCCCGCAGAGCAGCAAGACATAGCCACCGAGATCATCTCGAGATT	1213
OY	1651	GGACCGCATTTGAGGAGGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGG	1710
Db	1214	AGAAAGCATTTGAGGAAAGACCTGAGACCCTTGAAAGTGAATGATAGAAAACCGGAAT	1273
OY	1711	CAGCCAAAGAGAAAGCAGATGCGATCTATGATATGATTTGGTTCCCACTTTATCTCG	1770
Db	1274	CAGCCAAAGAAAGGCCGATGCACTCTCAACATGATAGGATATCCCAACTTCATCATGG	1333
OY	1771	AGCCCAAGACCTGATATGATTTTATGACGGGTACGAAATTTGGAAGATCTTCTTCC	1830
Db	1334	ATCCCAAGAGCTGGACAAAGTTTAAATGACTATACCTGACGTTTCAACCTCTACCTT	1393
OY	1831	AAACATGTTGAAATTTGTACAACTTCTCTGCCAAGTTATGAGTATGACGATCCGCAAGC	1890
Db	1394	AAATGCGATGGGTTTTCAACTTCTATGAGAGGTCACTGGCGATCAGCTCAGAAAG	1453
OY	1891	CTCCACGCCGAGACCAATGAGACATGACCCCCAGACAGTAAATGCTTACTTCCAA	1950
Db	1454	CCCCCAAGAGATCAGTGAGACATGACCCCGCCATGATGAAACGCTTACTTACCTGCCCA	1513
OY	1951	CTAAGAAAGATGCTGTTCCCGCTGGCATCTGCAAGCCCCCTTATGACCGCAAC	2010
Db	1514	CCAAAGATGAGATTTGTGTTTCCGGCCGGGATCTGCAAGACATTTCTACACAGCTCT	1573
OY	2011	ACCCCAAGGCCCTGAACTTCCGTGGCATCGGTGTGTCATGGGCCATGATGACGATG	2070
Db	1574	CACCAAGGCCCTTAACTTTGGTGGCATAGGTGTGCTGTGGGCCATAGCTGACTCATG	1633
OY	2071	CCTTGAATGACCAAGGGGCGAGTATGACAAAGAGGAACTGTGGGCGCTGTGGGCGAGA	2130
Db	1634	CTTTTGAATGATCAAGGACGGGAGTATGACAAAGAGGAACTTCCGCGCATGTGTGAAGA	1693
OY	2131	ATGATGCTCCTGGCAGCTTTCGCGAACCAACAGGCTGTGATGAGGAAACGATACATCAT	2190
Db	1694	ACTCATCTCGTGGAGGCTTTCAAGCGTCAAGACGATGATGGTATGACGATACAGCACT	1753
OY	2191	ACCAAGTCAATGGGAGAGAGGCTCAACCGGCGCCCAACGCTGGGGGAGAACTTGTGTACA	2250
Db	1754	ACAAGGTAAACGGGAGCGCGGTGAACGGGCGGCAACCTCGGGGAGAAATCGCCGACA	1813
OY	2251	ACGGGGGCTGAAGGCTGCTCAATGCTTACAAAGCATGTGCTGAGAAAGATGGGGAGG	2310
Db	1814	ACGGGGGCTCAAGGCGGCGCTTACGGGCTTACAAACCTGGGTGAAGAAAGACGGGCGTG	1873
OY	2311	AGCAGCAACTGCGACGCGGTGGGGCTCAACCAACACACAGCTCTTCTTCTGTGGATTTG	2370
Db	1874	AGCATCTGCTCCCAACCTCGGGGCTTCAACCAATAACACTCTTCTTCTCGGGCTTTG	1933
OY	2371	AGGTGTGGTGTCTCGGTCCGCAACACAGAGAGTCTCAAGAGGGGTGGTGAACGACCCC	2430
Db	1934	AGGTGTGGTGTCTCGGTCCGCAACCTGAGAGTCTCCAGAGAGGCTTCACTACCAATCCCC	1993
OY	2431	ACAAGCCCTGCGGCTTCCGCGTGTGGGCACTCTTCCAACTCCCGGTACCTTCTCGGCG	2490
Db	1994	ACAAGCCCTCTGCTTCCGGGCTATCGGCTCCCTCTCCAAATTCACAGAGATTCTCAGAAC	2053
OY	2491	ACTTGGCTGCTGCTGCTGCTCCCAATGAACCAAGAGGACAGTGTGTAAAGTGTGGTGA	2548
Db	2054	ACTTCCGCTGCGCACCTGCTTACCCATGAAACCGGCTTCAACAAGTGGCAAGTCTGGTGA	2111





1070 GCTCAGTCTATCTGGAATTACATGAGGAACTGGGGATGCTGGGGTGGGGCCAC 1129  
1083 CTTGGCAGCAATACAGGGGTGTTTCAATGAGCGAGTCTCAGCTCTGGGTG-----CAGA 1136  
1130 CTCACAGAGGAGCAGATGAGCAGGTGCTGAGATTGAGATACAGCTGGCCAAATCAC 1189  
1137 CGTGTGGAACAGAAAGGCCAAGAGATCTGCAAGTGAACAGAGAGTGGCCAAATCAC 1196  
1190 AGTGGCCAG-----GACCAAGGGCGCGACAGAGAGAAATCTACCAAGATGAGCAT 1243  
1197 TGTGTCAAGATATGACACCTACAGGCGAGATGTCAGTCCATGTACAAAGGTGAGCGT 1256  
1244 TTGGAGCTCAGAGCTCTGGGGCCCTTCATGAGACTGGCTTGAAGTCTGTCTTCTTCTG 1303  
1257 GGGGCAAGCTCAGAAATGACCCCTCCACTTGGCGGTG--AAAGTGGCTGTACACAGAT 1313  
1304 GTACCAATGAGATTGAGTGAATCTGAGCCTGTGTGTGTGTATGAGATGAGATTATTTGA 1363  
1314 CTTCCAGAGAGGACTTTCAGAGGAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1373  
1364 GCAAGTGTCAAGCTCATCAACGACAGAAACCAAGATCTGTAAACATTTACTGTATCTG 1423  
1374 GCAAGTGTCCAGCTCATCCGCTCCACACCCCAACGAGTGTGTGTGTGTGTGTGTGTGT 1433  
1424 GAACCTGGTCAAAAGCAACTCAAGCTGAGACCGAGCTTGTGAGTCTGTACAAAGAA 1483  
1434 GCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1493  
1484 GCTGTGAGAGACCTCTATGAGCACTAAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1543  
1494 GCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1550  
1544 CTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1603  
1551 GGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1610  
1604 TGAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1663  
1611 CTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1670  
1664 GGAAGCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1723  
1671 CCAAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1730  
1724 AGCAGATGCAATCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1783  
1731 GCTCCAGTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1790  
1784 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1843  
1791 GGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1847  
1844 TTTGTACAACTTCTGTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1903  
1848 CAGATGCGCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1907  
1904 CAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1963  
1908 CAGTGTGCTCTCCCTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1967  
1964 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2023  
1968 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2027  
2024 GAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2083  
2028 CAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2087  
2084 AGGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2143  
2088 GGGGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2147  
2144 AGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2203

2148 CCGCTTCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2207  
2204 GGAAGAGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2263  
2208 CCAAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2267  
2264 GGTGCTCTCAATGCTTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2323  
2268 GCTGAGCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2327  
2324 AGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2383  
2328 CCGGTCAAGTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2387  
2384 GGTGCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2443  
2388 CAAGCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2447  
2444 CTTCCGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2503  
2448 CTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2507  
2504 TGTGCGCTCCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2555  
2508 CAGAGACTACCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2559

RESULT 12  
US-09-704-611-4  
; Sequence 4, Application US/09704611  
; Patent No. 6548284  
; GENERAL INFORMATION:  
; APPLICANT: JCR Pharmaceuticals Co., Ltd.  
; TITLE OF INVENTION: Membrane-bound Metalloprotease and Soluble Secreted Form Thereof  
; FILE REFERENCE: GP30  
; CURRENT APPLICATION NUMBER: US/09/704,611  
; CURRENT FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 9  
; SEQ ID NO 4  
; LENGTH: 2823  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-704-611-4

Query Match 11.5%; Score 387.6; DB 4; Length 2823;  
Best Local Similarity 52.3%; Pred. No. 7,4e-83;  
Matches 1116; Conservative 0; Mismatches 949; Indels 69; Gaps 9;

527 CACCTGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 586  
430 CATCTGACACACCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489  
587 AGGAGTGAAGCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 646  
490 ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549  
647 CCCCCCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 706  
550 CGTGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 609  
707 GGCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766  
610 GGTATATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666  
767 GAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 826  
667 GAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726  
827 CCAAGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871  
727 TGAGCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786

QY 872 TACGGGCGCTGGGACGAGCACTTTATGAGGTGTGAAGCAGTAGCAGGACCTA 931  
 Db 787 GAACGAGACCAATGGGCTCTAAGTGGGAATCTGAGCGACATGGCTGTGTGAATCTGCA 846  
 QY 932 CAGGGCCACCCCAATCTTCAACG---TCTACATGAGTCCGACTTAAGATTCCACAG 988  
 Db 847 GTTCAACAGGCGGGTCTCTATGACCTCTTATCTGGAATGACACAGAACTCTCAACCG 906  
 QY 989 CAATGTTATCAGGTGAGCAAGTCTGGGCTTTCTGCTCTGCGGATTAATTA 1048  
 Db 907 GCATGTCATCTAATACCAAGCCACCTTGGGCAATCCCGGAGTAATAATTCCA 966  
 QY 1049 CAGACATGCCAATGAGAAAGTCTACTGCTATCTGATTAATGAGGAACTGGGAGT 1108  
 Db 967 GAGGAGCAACACCAACAGGTAAGGAAAGCTTACCGGAGTTCAATGACGTGAGCGAC 1026  
 QY 1109 GCTG-----CTGGGTGGGCGCGCCACCTCCACGAGGAGCAGATGCA 1150  
 Db 1027 TATGCTTAGAAGAACCAAGAACTGTCCAGAGAGCGCATGGGTGGGAGGAGATGGC 1086  
 QY 1151 GCAGGTCTGAGTGTGAGTACAGCTGGCCACATACAGTGTCCCAAGACCAAGCGCG 1210  
 Db 1087 GAGGTGTCTGGAATGAGACGATCTGGCCACGCAAGTCCCGCAGAGAAAGCA 1146  
 QY 1211 CGACGAGAGAAAGTCTACCAAGATGAGCAATTTGAGAGTGTGAGGCTGTGGCGCCCTC 1270  
 Db 1147 TGAATGACCTGCGCTGTACCAAGAAATGACCTGATGAGCTTACAGAAAGTTGGTCT 1206  
 QY 1271 CATGG-----ACTGGCTTGAATCTCTGCTTCTTCTGCTGCAAC-----ATTGAGTT 1318  
 Db 1207 GAGGGGGTTTAATCTGACCTCTCTTCAATCAAAAGTGTGTCTGTGAGAGTCAGACT 1266  
 QY 1319 GAGTGAATCTGAGCTGTGTGTGTGTATGAGATGATTAATTTGACAGAGTGTCAAGCT 1378  
 Db 1267 GTTCCAGAAAGAGAGGTGTGTGTATGAGCAATCCCTTACCTGAGATCTGAGAGTAT 1326  
 QY 1379 CATCAACCGCAGGAAACCAAGATCTGAAATTAATCTGATCTGAAACCTGGTGAACAA 1438  
 Db 1327 CATTTGATGCTACTCAGACGACATGCAAACTGCAAACTGATGATGGGCTGTGGTCTGA 1386  
 QY 1439 GACAACTCAAGCTGTGAGCCGACGCTTTGAGTCTGCAAGAGAAAGTGTGAGACCT 1498  
 Db 1387 TCGAATTTGGCAGCTGAGCCAGAGATTCAAGAGGGCGTGTGAGCTACGCAAGGCGCT 1446  
 QY 1499 CTATGCACTTAAGAAGTCTGTGTGCGAGGTGAGCACTGCAATCTCAACAGAGTGA 1558  
 Db 1447 GTACGGCAGCAGCGTGTGAGAGGTGAGCTGGCCAGAGTGTGTGATGTCTCAACAGTAA 1506  
 QY 1559 CGCCCTTGGCTTTGGGGTCCCTCTGTGAGAGGCGACGTTTGAACGGCAAGCA 1618  
 Db 1507 CATGAGAGC--GCCGTGGGCTCCCTCTACATCAACGGGCTTCTCAAGAGCAGCA 1563  
 QY 1619 AGAAATTTGCAAGAGGATGATCAGCAAAATCCGACCGCATTTGAGGAGGCTCTGGACA 1678  
 Db 1564 GAGCAGGTGACAGAGCTGATGAGAAAGTAAGTCCGTGTGTGTGATTAACCTGATGA 1623  
 QY 1679 GCTGTTTGTGATGATGAGAAACCGCCAGGACGCAAGCAAGAAAGCAGATCCATCTA 1738  
 Db 1624 GCTGAAGTGTGATGAGAGGAATCCAAAGAAAGGCGCCAGGAAGGCGCATGATATACG 1683  
 QY 1739 TGAATGATTTGTTTCCAGACTTTATCCGAGAGCC-----AAAGAGTGTGATGT 1792  
 Db 1684 GGAACGATTTGGCTTACCTGACTACATTTTGAAGATTAACAATTAACCTGATGAGGA 1743  
 QY 1793 TTAATGACGGTACGAATTTCTGAAGATCTTTCTTCAAAACATGTTGAATTTGTACAA 1852  
 Db 1744 ATACTCAAGTTTACCTTTATGAGAGCTGTATTTTGAAGAGACTTCAGAACTCA 1803  
 QY 1853 CTCTCTGCGCAAGTTATGCTGACAGCTCCGCAAGCTCCACGCGGAGACCAATGTGAG 1912  
 Db 1804 GAACAATGCCCAAGAGGCTCTCAAGAAAGCTTCCGGAAGAGTGAACCAAGATCTCTGAT 1863  
 QY 1913 CATGACCCCCCAAGTGAATGCTACTACTTCAACTAAGATGAATGATGTCTTCC 1972

Db 1864 CATGGGGGCTGAGTGTGATGATCTACTCTCCCAACAGAAACCAAGATGTCTTCC 1923  
 QY 1973 CGCTGATCTCTGAGGCGCCCTTTCTATGCGCGCAACCAACCCAGGCTGAACTTCCG 2032  
 Db 1924 AGCAGGGAATCTCAACCGCCCTTCTTCAAGCAAGACCAACAGCTTGTGAATTTGG 1983  
 QY 2033 TGGCATGTGTGTGATGAGGCGCATAGTTGAAGCATGCTTGTGAATGAACCAAGGCGCA 2092  
 Db 1984 GGGCATGTGTGTGATGAGGCGCATAGTTGAAGCATAGTTGAATGAATGATGATGATGAT 2043  
 QY 2093 GTATGACAAAGAGGAACTGTGCGCTGTGTGGCAAAATGATGCTTGTGCAACCTTCCG 2152  
 Db 2044 CTTTGAACAGAAAGGCAACATGCTGATCTGTGTGATTAATCTTCCGCGCGGCACTTCCA 2103  
 QY 2153 GAACCAACGGCTGTGATGAGGAAACATGATCAATCAATAC-----CAGTCAATGG 2203  
 Db 2104 ACAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163  
 QY 2204 GAGAGGCTCAACGGCGCGCAAGCGTGGGGAGAAATTTGCTGACAAACGGGGGCTGAA 2263  
 Db 2164 CCAAGATGTGAAGGATTCAGTTCTCTGGGGAGAACTTTGCGCAACGAGGATGTGCG 2223  
 QY 2264 GGCTGCTCAATGCTTTAACAAGATGCTGAGAAAGCATGAGGAGAGAGCAATGCGC 2323  
 Db 2224 ACAGGATACAGGCTTACTCTGATGCTGTGCTGATGAGCGGAAAGATGAGCACTGCC 2283  
 QY 2324 AGCGTGGGCTGACCAACCAACAGCTCTTCTGTGTGAGATTTGCCAGGTGTGTCTC 2383  
 Db 2284 GGAATGAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343  
 QY 2384 GGTCCGCAACCAAGAGCTCTACAGAGGGCTGTGTGATGATGATGATGATGATGATGATGAT 2443  
 Db 2344 GTCTATAGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2403  
 QY 2444 CTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2503  
 Db 2404 GTACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2463  
 QY 2504 TGTGGCTCCCGCATGAAACCCAGGAGCTGTGTGAGGTGTGTGTGTGTGTGTGTGTGTGT 2563  
 Db 2464 ACAGGCAAGCCCATCATCACCCATGAAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2523  
 QY 2564 AGAAATGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2597  
 Db 2524 TGTGTGGGCCCAAGCCCGCCAGCCAGAGATGTGC 2557

## RESULT 13

US-09-704-611-3  
 ; Sequence 3, Application US/09704611  
 ; Patent No. 6548284  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JCR Pharmaceuticals Co., Ltd.  
 ; TITLE OF INVENTION: Membrane-bound Metalloprotease and Soluble Secreted Form Ther  
 ; FILE REFERENCE: GP30  
 ; CURRENT APPLICATION NUMBER: US/09/704,611  
 ; CURRENT FILING DATE: 2000-11-03  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SEQ ID NO 3  
 ; LENGTH: 2892  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 US-09-704-611-3

Query Match 11.5%; Score 387.6; DB 4; Length 2892;  
 Best Local Similarity 52.3%; Pred No. 7.5e-83;  
 Matches 116; Conservative 0; Mismatches 949; Indels 69; Gaps 9;  
 QY 527 CACTGCTTACAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 586  
 Db 499 CATCTGACCAACCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 558

QY 587 AGGGGTGAGCCCTGTTGAGGACTTTTACGATTCTCTGTTGGGGGCTGATTGAGGAA 646  
 DB 559 ATGAGAGAACCCCTGTGAAAACTTACAGTAAGCTGCGAGAGCTGGCTGAGGCCA 618  
 QY 647 CCCCTGCGGATGAGGGGCTTCTGCTGGAACAACCTTCAACAGCCTTGGAGCCAAAACA 706  
 DB 619 CGTATCTCCAGAACCAACCTCCGATACAGGCTTTTGAATCTGTGGGGAGCAAGCTGGA 678  
 QY 707 GGGCATATGAGAACCTGCTTGAATAAACCAACCTTCACTCCAGCACTGAACCTGAGCA 766  
 DB 679 GGTATATCTTCAAAAGGGGTGTGAGGATTCACCTTCCAGCATGCG---CCGGCCGTGGA 735  
 QY 767 GAAGACACAGCGCTTACCTATCTTGGCTTACAGTGGAGCGCATTTGAGGAGCTGGAGAGC 826  
 DB 736 GAAGGCGAAGACATATATGCTCTCTGATGAACCAAGTGTGATGAGAGAGAGACTC 795  
 QY 827 CCAGCACTGAGAGACCTCATTTGAGAGATTGTTGGTGG-----AACAAT 871  
 DB 796 TGAAGCCCTGTGAGGCTTTAAATAATGTAAGAGGTGGCTGTGGCATTTGATTAAGTG 855  
 QY 872 TACGGGGCCCTGGAGCCAGAGCACTTTATGAGGTGTTGAAGCGAGTACAGAGACTTA 931  
 DB 856 GAACGAGACCATGGGCTTCAAGTGGGAATGAGCCAGAGTTGGCTGTGTGAACTTCGA 915  
 QY 932 CAGGGCCACCCCAATTCTTACCG---TCTACATCAGTGGCCGACTTAAAGATTCAACAG 988  
 DB 916 GTTCAACAGCGGGGCTCTCATCTGACTTTTCACTGTGAATGAGACCAAGAACTTCAAGC 975  
 QY 989 CAATGTTATCCAGTGTGACAGTCTGGGCTCTTCTGCGCTCTCGGGATTACTTAA 1048  
 DB 976 GCATGTCATCTATACAGACCAAGCCACCTTGGGATCCATCCGGAGTACTTATTTCCA 1035  
 QY 1049 CAGAACTGCCAATGAGAAAGTGTCTCACTGCTTATCTGATTAATGAGAGAACTGGGAGAT 1108  
 DB 1036 GAGGACCAACCAACCAAGGTAAGGAAAGCTTACCCGAGTTCAATGACGTGAGGCGAC 1095  
 QY 1109 GCTG-----CTGGGTGGGGCGGCCACCTCCACGAGGGAGGAGATGCA 1150  
 DB 1096 TATGCTTGAAGAAAGACCAAGAACTGTCCAGAGAGAGGCGCATGTGTGGAGAGATGCG 1155  
 QY 1151 GCAAGTGTCTGAGTGTGAGTACAGCTGAGCCAAATCAACAGTGGCCCAAGACCAAGCGGCG 1210  
 DB 1156 GAGGTGTCTGAACTGAGAGCGATCTGGCCAAAGCCACAGTCCCCAGAGAAAGAGCA 1215  
 QY 1211 CGAGAGAGAAATATCTACCAACAAGATGAGATTTGGAGACTGAGGCTGTGGCGCCCTC 1270  
 DB 1216 TGAATGTCACTGCCCTGTACCAAGAAATGACCTGATGAGCTTACAGGAAAGTTGTGCT 1275  
 QY 1271 CATGG-----ACTGCTGAGTTCTGTCTTCTTCTGTGAC-----ATTGAGTT 1318  
 DB 1276 GAAAGGGTTTAACTGAGACTCTTTCAACAAGAGTGTGTCTTCTGTGAGAAATGCAAGCT 1335  
 QY 1319 GAGTGACTGTAGCTGTGTGTGTATGAGATGATTTATTTGACAGAGGTGTCAAGCT 1378  
 DB 1336 GTTCCAGATGAGAGGTGTGTGTATCGGATCCCTTACCTGGAATCTGAGAGATAT 1395  
 QY 1379 CATCAACCGACGAGAACCAAGACTCTGAACTTAACTGATCTGGAACCTGTGTGAAAA 1438  
 DB 1396 CATTGATAGCTTACTAGACAGAACCATGAGAACTTCTGTATGTGGGCTGTGTGTGAGA 1455  
 QY 1439 GACAACTCAAGCTGAGCCGACGCTTTGAGTGTGACAAAGAAAGTGTGTGAGAACCT 1498  
 DB 1456 TCGAATTGGCAGCTGTAGCCAGAGATTCAAAGAGGCCGTGTGTGACTTACCGCAAGGCGCT 1515  
 QY 1499 CTATGCACTTAAAGAGTCTGTGTGTGAGAGTGTGAGAGCTGTCACTCAACCGAGATGA 1558  
 DB 1516 GTACGGACACGCGTGAAGAGGTACGCTGGCGAGATGTGTGAGTATGTCAACAGTAA 1575  
 QY 1559 CGCCCTTGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1618  
 DB 1576 CATGGAAGAGC---GCCGTGGGCTTCCCTTCAATCAACCGGGCTTCTTCCAAAGGACAGCA 1632  
 QY 1619 AGAAATTGCAAGAGGGGATGATCAGCAAAATCCGAGCCGCAATTTGAGAGAGCCCTGGGACA 1678

DB 1633 GAGCAACGTCAGAGAGCTGATTGAGAGATTAAGTCCGTTGTGTGATTAACCTGATGA 1692  
 QY 1679 GCTGTTTGAATGATGAGAGAACCCGACGACGCAAGAGAGAAAGCATGCTCTTA 1738  
 DB 1693 GCTGAATGATGATGAGAGAGAAATCCAAAGAAAGGCCGAGAAAGGCATGAATATAGC 1752  
 QY 1739 TGATATGATTGTTTCCGAGCTTTATCCTGAGGCC-----AAAGACTGATGATGT 1792  
 DB 1753 GGAACAGATTGGCTACCTGATCTTACATTTTGAAGATTAACAATTAACCTGATGAGGA 1812  
 QY 1793 TTATGACGGGTACGAAATTTGAAATTTCTTCTTCCAAAACATGTTGAATTTGTACA 1852  
 DB 1813 ATATCTCAATTTGACTTTTATGAGGACCTGATATTTTGAAGACGACTTCAAGACCTCAA 1872  
 QY 1853 CTCTCTGCAAGGTTATGCTGACCAAGCTCCGCAAGCTCCAGCCGAGACCATGTGGAG 1912  
 DB 1873 GAACATGCCCAGAGAGGCTTCAAGAAAGCTTGGGAAAGGTGAGACGAATCTCTGAT 1932  
 QY 1913 CATGACCCCCAGACAGTAAAGCTTACCTTCCAACTTAAGAAATGAGATGCTTCC 1972  
 DB 1933 CATGGGGCTGCAATGTGATTAATGATTTTATCTCCAAACAGAAACAGATGCTTCC 1992  
 QY 1973 CGCTGCAATCTTGCAGGCCCCCTTCTATGCCCCGCAACCAAGCCGCTGAACTTCCG 2032  
 DB 1993 AGCAGGATTTCTCAGCGCGCTTCTTCAAGCAAGACCAACCAAGTCTTGAATTTGG 2052  
 QY 2033 TGGCATGCGTGTGTATGAGGCAATGATGTAAGCATGCTTGTGATGACCAAGGCGCA 2092  
 DB 2053 GGGCATCGGAGATGTGATTTGGGCAAGATTCACAGCGCTTGTGATTAATGTGCTGA 2112  
 QY 2093 GTATGACAAAGAGGAACTGTGGGCCCTGGGAGCAATGATGTCCTGGAGCTTCCG 2152  
 DB 2113 CTTTGAAGAAACGGAACATGTGATCTGTGAGTAACTTCTGAGCCGCACTTCCA 2172  
 QY 2153 GAACCAACGCGCTGTGAGAGAAACATGATCAATCAATAC-----CAGTCAATG 2203  
 DB 2173 ACAGCATGCAATGATGATGATCATGATCAGAACGCAACTTCTTGGGAATGACAGACA 2232  
 QY 2204 GAGAGAGCTCAACGCGCCGACAGCTGGGGGAGAAATTTGCTGACAAAGGGGGGTGAA 2263  
 DB 2233 CCAGAAATGGAACGGAATTCAGTTCCTGGGAGAAATTTGCGACCAAGAGGTGTGG 2292  
 QY 2264 GGTGCTTCAATGTCTTAAAGACATGGCTGAGAAAGCATGGGAGAGAGACAGCACTGCC 2323  
 DB 2293 ACAGGATTTCAAGGCTTACTAGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2352  
 QY 2324 AGCCGTGGGGCTCAACCAACCAAGCTCTTCTGTGGATTTGCGAGGTGTGTGCTC 2383  
 DB 2353 GGGACTGAACCTGACCTTAGCCAGCTTTTCTTCACTCACTATGCCCAGGTGTGTGTG 2412  
 QY 2384 GGTCCGACACCAAGAGAGCTTCAAGAGGGGCTGTGATCCGACCCCAAGCCCTGCCG 2443  
 DB 2413 GTCTTATAGGCGGAGTTTGGCGTCCAGTCACTCAAGAGAGCTTCAAGCTTCTTAA 2472  
 QY 2444 CTTCCGCTGTGGGCACTCTTCCAACTCCGCTGACTTCTGCGGCACTTGGGCTGCC 2503  
 DB 2473 GTACAGGATGTGTGAGCTTCACTACAGAACTGCGAGCTTCTGTAGGCAATTCACGCCC 2532  
 QY 2504 TGTGCTCCGCCCATGAACCCAGAGGAGCTGTGTGAGGTGTGTGACCTGTGATCAAGGG 2563  
 DB 2533 AGGAGGAGCCCATCAACCCATGAAGAGATGTGCACTGTGTAGCCAAAGGTGAGCTA 2592  
 QY 2564 AGAAATGCCAGTGTTCACCAAGACTGTGGGCAAGC 2597  
 DB 2593 TGTGCGGCCCAAGCGCCCGCAACCCAGAGGTGCG 2626

RESULT 14  
 US-08-646-273-13  
 ; Sequence 13, Application us/08646273  
 ; Patent No. 606502  
 ; GENERAL INFORMATION:





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XX (INCY-) INCYTE PHARM INC.  
XX Walker MG, Volkmutch W, Klingler TM;  
XX WPI; 2000-375619/32.  
XX  
PT A new purified polynucleotide comprising a gene that is coexpressed with  
PT neurotransmitter-processing-specific genes in biological samples for  
PT diagnosing, treating or preventing neurological and hormone-related  
PT diseases.  
XX  
PS Claim 2; Page 32-33; 36pp; English.  
XX  
CC The present invention describes a purified polynucleotide comprising a  
CC gene that is coexpressed with one or more neurotransmitter-processing-  
CC specific genes in biological samples. The neurotransmitter-processing-  
CC specific genes are L-tyrosine hydroxylase (TH), aromatic amino acid  
CC decarboxylase (AADC), dopamine beta-hydroxylase (DBH), nicotinic  
CC acetylcholine receptor alpha3 subunit precursor (nAChR-alpha3),  
CC secretogranin I and II, Rab3a, human cocaine and amphetamine regulated  
CC transcript (hCAR), vesicular monoamine transporter 1 (VMAT1), and ARX  
CC homeodomain protein. The present sequence represents a neurotransmitter  
CC associated nucleotide sequence from the present invention. The  
CC polynucleotides from the present invention can have antiparkinsonian,  
CC neuroleptic, anticonvulsant, nootropic, tranquilizer, neuroprotective,  
CC cyostatic, antidepressant, antidiabetic, gynecological and  
CC immunosuppressive activities. They can be used for diagnosing, treating,  
CC preventing or evaluating therapies for neurological and hormone-related  
CC diseases, particularly Parkinson's disease, schizophrenia, epilepsy,  
CC female reproductive disorders and attention deficit disorder. The gene  
CC products are therapeutic proteins and targets of therapeutics against the  
CC diseases  
XX  
SQ Sequence 3000 BP; 672 A; 845 C; 858 G; 625 T; 0 U; 0 Other;  
Query Match 87.6%; Score 2958.2; DB 3; Length 3000;  
Best Local Similarity .99.4%; Pred. No. 0;  
Matches 2980; Conservative 0; Mismatches 18; Indels 1; Gaps 1;  
QY 360 CTCTGCTCTAGAGCTATGATGAGGATTCAGAGGGGACAGAGAGCTGTAGGCTCAGC 419  
DB 2 CTGGGAGCTGGAGCAAGTGGGATTCAGAGGGGACAGAGAGCTGTAGGCTCAGC 61  
QY 420 ACCGAGCTGAGAGCTGCTTACAGAGGCTCTTACAGAGGCTCTTACAGAGGCTCTTACAG 479  
DB 62 ACCGAGCTGAGAGCTGCTTACAGAGGCTCTTACAGAGGCTCTTACAGAGGCTCTTACAG 121  
QY 480 TGCCTTGTGAGCCCTAGAGGCTCAAGTACAGAGAGCCATCCAGAGAGCTCTTACAG 539  
DB 122 TGCCTTGTGAGCCCTAGAGGCTCAAGTACAGAGAGCCATCCAGAGAGCTCTTACAG 181  
QY 540 GAGGCTGAGCTTGTGAGTGGCTGAGAAATCTGTGAGTCCCTGAGCCGAGGAGTGAAGCCC 599  
DB 182 GAGGCTGAGCTTGTGAGTGGCTGAGAAATCTGTGAGTCCCTGAGCCGAGGAGTGAAGCCC 241  
QY 600 TGTGAGGAGCTTTTACAGAGTCTCTGTGAGGAGCTGAGTTGAGAGAGAGCCCTGAGCCGAT 659  
DB 242 TGTGAGGAGCTTTTACAGAGTCTCTGTGAGGAGCTGAGTTGAGAGAGAGCCCTGAGCCGAT 301  
QY 660 GGGGCTTCTGAGTGAACACCTTCAAGAGCTCTGAGAGCAAAACAGAGGCTATCTAGAG 719  
DB 302 GGGGCTTCTGAGTGAACACCTTCAAGAGCTCTGAGAGCAAAACAGAGGCTATCTAGAG 361  
QY 720 CACCTGCTTGAACACACCTTCAAGAGCTCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 779  
DB 362 CACCTGCTTGAACACACCTTCAAGAGCTCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 421  
QY 780 TTCTACTATCTTCTGAGTGAAGAGTGAAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 839  
DB 422 TTCTACTATCTTCTGAGTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481  
QY 840 GACCTCATGAGAGAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899

DB 482 GACCTCATGAGAGAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541  
QY 900 ATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959  
DB 542 ATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601  
QY 960 ATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019  
DB 602 ATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661  
QY 1020 TTTTGGCCCTCTGAGAGATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079  
DB 662 TTTTGGCCCTCTGAGAGATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721  
QY 1080 TATCTGAGATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139  
DB 722 TATCTGAGATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781  
QY 1140 GAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199  
DB 782 GAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841  
QY 1200 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259  
DB 842 GAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901  
QY 1260 CTGGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319  
DB 902 CTGGGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961  
QY 1320 AGTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379  
DB 962 AGTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021  
QY 1380 ATCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1439  
DB 1022 ATCAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081  
QY 1440 ACAAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1499  
DB 1082 ACAAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141  
QY 1500 TATGAGCACTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1559  
DB 1142 TATGAGCACTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201  
QY 1560 GGCCTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619  
DB 1202 GGCCTTGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261  
QY 1620 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679  
DB 1262 GAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1321  
QY 1680 CTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1739  
DB 1322 CTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381  
QY 1740 GATATGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1799  
DB 1382 GATATGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1441  
QY 1800 GGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1859  
DB 1442 GGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501  
QY 1860 GCGAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1919  
DB 1502 GCGAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1561  
QY 1920 CCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1979



Db 1562 CCCAGACAGTGAATGCTACTACTCTCACTCAACTAAGATGATCTGCTCCCGCTGAC 1621  
Qy 1980 ATCTGAGAGGCCCCCTTCTATGCCCCGGAACCAACCCCAAGGCTCTGAATCTTGCGGATC 2039  
Db 1622 ATCTGAGAGGCCCCCTTCTATGCCCCGGAACCAACCCCAAGGCTCTGAATCTTGCGGATC 1681  
Qy 2040 GGTGGGTCAATGAGGAGGAGTGAAGCATGATGAGCTTTGATGACCAAGGCGCAGATGAC 2099  
Db 1682 GGTGGGTCAATGAGGAGGAGTGAAGCATGATGAGCTTTGATGACCAAGGCGCAGATGAC 1741  
Qy 2100 AAGAAAGGAACCTGCGGCTGCTGAGTGAAGTATGCTGCGACGCTTCCGAAACAC 2159  
Db 1742 AAGAAAGGAACCTGCGGCTGCTGAGTGAAGTATGCTGCGACGCTTCCGAAACAC 1801  
Qy 2160 ACGGCTGCAATGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2219  
Db 1802 ACGGCTGCAATGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 1861  
Qy 2220 CGCAGACGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2279  
Db 1862 CGCAGACGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 1921  
Qy 2280 TACAAAGCATGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2339  
Db 1922 TACAAAGCATGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 1981  
Qy 2340 AACCAACAGTCTTCTTCTGCGGATTTGCGGAGTGTGCTGCTGCTGCGCAACCAAG 2399  
Db 1982 AACCAACAGTCTTCTTCTGCGGATTTGCGGAGTGTGCTGCTGCTGCGCAACCAAG 2041  
Qy 2400 AGCTCTCAGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2459  
Db 2042 AGCTCTCAGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2101  
Qy 2460 ACTCTCTCAACTCTCCGTGATCTTCTGCGGATTTGCGGAGTGTGCTGCTGCTGCGCAACCAAG 2519  
Db 2102 ACTCTCTCAACTCTCCGTGATCTTCTGCGGATTTGCGGAGTGTGCTGCTGCTGCGCAACCAAG 2161  
Qy 2520 AACCCAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2579  
Db 2162 AACCCAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2221  
Qy 2580 CACCAAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2639  
Db 2222 CACCAAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2281  
Qy 2640 ATGCAAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2699  
Db 2282 ATGCAAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2341  
Qy 2700 TCATATCAATGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2759  
Db 2342 TCATATCAATGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2401  
Qy 2760 ATTCACTGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2819  
Db 2402 ATTCACTGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2461  
Qy 2820 TTCCATAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2879  
Db 2462 TTCCATAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2521  
Qy 2880 GGGCTGCTGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2939  
Db 2522 GGGCTGCTGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2581  
Qy 2940 TTCCAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2999  
Db 2582 TTCCAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2641  
Qy 3000 CGGGCTACCCCACTCAATGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 3059  
Db 2642 CGGGCTACCCCACTCAATGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2701

Qy 3060 CTTCACTGACAGTCTCTAGTGAAGGCCAAGGAGCTCTGAAAGGCTCTGCTGCCACTG 3119  
Db 2702 CTTCACTGACAGTCTCTAGTGAAGGCCAAGGAGCTCTGAAAGGCTCTGCTGCCACTG 2761  
Qy 3120 TTTCCCTGAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 3179  
Db 2762 TTTCCCTGAGCTGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2821  
Qy 3180 GGCACAAAGC-TTAAAGCAATGATTATTTCTCTGCAAAAGCAGAGGAGTGAAGC 3238  
Db 2822 GGCACAAAGC-TTAAAGCAATGATTATTTCTCTGCAAAAGCAGAGTGAAGC 2881  
Qy 3239 AGGAAAGGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 3298  
Db 2882 AGGAAAGGAGGAGGAGTGAAGTATGCTGAGTCAATGAGTGAAGGAGGCTCAAGGC 2941  
Qy 3299 GCCCTTATAGAACCTGTGCAATGAAGCAGATGATCGTCAAAAAA 3357  
Db 2942 GCCCTTATAGAACCTGTGCAATGAAGCAGATGATCGTCAAAAAA 3000

RESULT 3  
AAZ34326  
ID AAZ34326 standard; cDNA; 2602 BP.  
XX  
AC AAZ34326;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PR0403 nucleotide sequence.  
XX  
KW Human; PRO, EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX  
OS Homo sapiens.  
XX  
PN W09946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99NO-US005028.  
XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
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PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
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 PR 22-MAY-1998; 98US-0086486P.  
 PR 28-MAY-1998; 98US-0087098P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 30-MAY-1998; 98US-0087208P.  
 PR 30-MAY-1998; 98US-0094651P.  
 PR 11-SEP-1998; 98US-0100038P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX  
 DR WPI, 1999-551358/46.  
 XX P-PSDB; AAY41774.  
 XX  
 PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders.  
 XX  
 PS Claim 2; Fig 224; 530pp; English.  
 XX

CC The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as sources  
 CC of probes, primers, for chromosome mapping, and for generation of  
 CC antisense sequences. They can also be used to create transgenic animals.  
 CC The proteins can be used to treat a variety of diseases and disorders,  
 CC depending on their function. Diseases that may be treated include blood  
 CC coagulation disorders, cancers and cellular adhesion disorders. They may  
 CC also be used to raise antibodies. AA23891 to AA23438, and AAY41685 to  
 CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
 CC exemplification of the present invention  
 XX

SQ Sequence 2602 BP; 577 A; 737 C; 767 G; 521 T; 0 U; 0 Other;

Query Match 72.9%; Score 2461.2; DB 2; Length 2602;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	360	CTCTGCTCTAGAGCTATGCTGGGATTCAGAAAGGAGCAAGACGCTTTAGGCTCAGCC	419
DB	121	CTGGAGAGCTGGAGCAAGCTGGGATTCAGAAAGGAGCAAGACGCTTTAGGCTCAGCC	180
QY	420	ACGCACTGAGCTGGCTTTAGCAGGTGCTCTTACTGCTGGCTTCACTGCTTCTGGGC	479
DB	181	ACGCACTGAGCTGGCTTTAGCAGGTGCTCTTACTGCTGGCTTCACTGCTTCTGGGC	240
QY	480	TGCTTGTGAGGCTTGGGCTCAGTACAGAGACCCATCCCAAGCACTGCTTACA	539
DB	241	TGCTTGTGAGGCTTGGGCTCAGTACAGAGACCCATCCCAAGCACTGCTTACA	300
QY	540	GAGGCTGATTCAGTGGCTGAGAAATCTGAGTCTCTGAGCCGAGGCTGAGCCCC	599
DB	301	GAGGCTGATTCAGTGGCTGAGAAATCTGAGTCTCTGAGCCGAGGCTGAGCCCC	360
QY	600	TGTGAGAGCTTTTACCAAGTTCCTGGGGCTGGATTCGAGGAAACCCCTGGCCGAT	659
DB	361	TGTGAGAGCTTTTACCAAGTTCCTGGGGCTGGATTCGAGGAAACCCCTGGCCGAT	420
QY	660	GGGCGTTCTCGCTGGAACACTTCAACAGCTCTGAGCAACAAACGAGCCATCTGAAG	719
DB	421	GGGCGTTCTCGCTGGAACACTTCAACAGCTCTGAGCAACAAACGAGCCATCTGAAG	480
QY	720	CACCTGCTTGAAGAACCACTTCAACAGCTCTGAGCAACAAACGAGCCATCTGAAG	779
DB	481	CACCTGCTTGAAGAACCACTTCAACAGCTCTGAGCAACAAACGAGCCATCTGAAG	540
QY	780	TTCCTACCTTCTTGGCTTACAGGTGAGGCGCATTTGAGAGCTGGAGCCAGCACTGAGA	839
DB	541	TTCCTACCTTCTTGGCTTACAGGTGAGGCGCATTTGAGAGCTGGAGCCAGCACTGAGA	600
QY	840	GACCTCATTTGAGAGATTTGGTGGTGAACATTAACGGGCGCTGGAGCCAGCACTTT	899
DB	601	GACCTCATTTGAGAGATTTGGTGGTGAACATTAACGGGCGCTGGAGCCAGCACTTT	660
QY	900	ATGAGAGTGTGAAGCACTGAGGAGCTTACAGGCGCAACCCCATTTCTTCACTGTAC	959
DB	661	ATGAGAGTGTGAAGCACTGAGGAGCTTACAGGCGCAACCCCATTTCTTCACTGTAC	720
QY	960	ATGAGAGTGTGAAGCACTGAGGAGCTTACAGGCGCAACCCCATTTCTTCACTGTAC	1019
DB	721	ATGAGAGTGTGAAGCACTGAGGAGCTTACAGGCGCAACCCCATTTCTTCACTGTAC	780
QY	1020	TTTCTGCTTCTGGGATTAATTAACAGAACTGCAATGAGAAATGCTCACTGCC	1079
DB	781	TTTCTGCTTCTGGGATTAATTAACAGAACTGCAATGAGAAATGCTCACTGCC	840
QY	1080	TATCTGATTAATTAATGAGAGAACTGGGATGCTGGTGGGCGGCCCACTTCAGAGG	1139
DB	841	TATCTGATTAATTAATGAGAGAACTGGGATGCTGGTGGGCGGCCCACTTCAGAGG	900
QY	1140	GAGCAATGAGAGAGTGTGAGAGTGTGAGATACAGCTGGCCCAATCAAGTGGCCAG	1199
DB	901	GAGCAATGAGAGAGTGTGAGAGTGTGAGATACAGCTGGCCCAATCAAGTGGCCAG	960

QY	1200	GACCAAGCGGCGCGACGAGAGAAATCTACCAACAAGAGACATTTGCGAGCTCGAGCT	1253
Db	961	GACCAAGCGGCGCGACGAGAGAAATCTACCAACAAGAGACATTTGCGAGCTCGAGCT	1020
QY	1260	CTGGGCGCCCTCCATAGACTGGCTTGAGATTCTCTGCTTTCTTGCTGTCACCATTTGAGATTG	1319
Db	1021	CTGGGCGCCCTCCATAGACTGGCTTGAGATTCTCTGCTTTCTTGCTGTCACCATTTGAGATTG	1080
QY	1320	AGTGACTGTAGCCCTGTGTGTGTATGGATGTGATTTTTCAGCAGGTGTGACGCTC	1379
Db	1081	AGTGACTGTAGCCCTGTGTGTGTATGGATGTGATTTTTCAGCAGGTGTGACGAGCTC	1140
QY	1380	ATCAACCGCACGGAACCAAGCATCTGTAAACAATTACTGATCTGGAACTTGTGTCAAAAG	1439
Db	1141	ATCAACCGCACGGAACCAAGCATCTGTAAACAATTACTGATCTGGAACTTGTGTCAAAAG	1200
QY	1440	ACAACCTCAAGCCTTGAGACGGAACGCTTTGAGTGTGACAAGAGAGAGCTGTGAAACCTC	1499
Db	1201	ACAACCTCAAGCCTTGAGACGGAACGCTTTGAGTGTGACAAGAGAGAGCTGTGAAACCTC	1260
QY	1500	TATGGCATTAGAAAGTCTGTGTGTGCGAGGTGTGAGACCTGCAATCTCCAAACACGAGATGAC	1559
Db	1261	TATGGCATTAGAAAGTCTGTGTGTGCGAGGTGTGAGACCTGCAATCTCCAAACACGAGATGAC	1320
QY	1560	GCCCTTGCCCTTTGCTTTTGGGGTCCCTCTCTGTGTGAAGGCGACAGTTTGACCCGCAAAAGCAA	1619
Db	1321	GCCCTTGCCCTTTGCTTTTGGGGTCACTCTCTGTGAAGGCGACAGTTTGACCCGCAAAAGCAA	1380
QY	1620	GAAATTGACAGGGGGATGATCAGGGGAAATCCGGACCCGATTTGAGAGGGCCCTGTGGACAG	1679
Db	1381	GAAATTGACAGGGGGATGATCAGGGGAAATCCGGACCCGATTTGAGAGGGCCCTGTGGACAG	1440
QY	1680	CTGGTTTGATGTAGTAGAAGAACCCGCGACGACGCAAGAGAAAGCAGATGCCATCTAT	1739
Db	1441	CTGGTTTGATGTAGTAGAAGAACCCGCGACGACGCAAGAGAAAGCAGATGCCATCTAT	1500
QY	1740	GATATGATTGGTTTCCAGACTTTATCTGTGAGCCCAAGGCTGTGATGATGTTTATGAC	1799
Db	1501	GATATGATTGGTTTCCAGACTTTATCTGTGAGCCCAAGGCTGTGATGATGTTTATGAC	1560
QY	1800	GGGTACGAAATTTCTGAGATCTTTTCTTCCAAACATGTGAAATTTGTAACACTTCTCT	1859
Db	1561	GGGTACGAAATTTCTGAGATCTTTTCTTCCAAACATGTGAAATTTGTAACACTTCTCT	1620
QY	1860	GCCAAAGTTTATGAGTCAACAGCTCCGCAAGCCTCCACGCGACACCAAGTGAAGATGAC	1919
Db	1621	GCCAAAGTTTATGAGTCAACAGCTCCGCAAGCCTCCACGCGACACCAAGTGAAGATGAC	1680
QY	1920	CCCCAGACAGTGAATGCTCTACTACCTTCCAACTAGAAATGAGATCGTCTTCCCGCTGGC	1979
Db	1681	CCCCAGACAGTGAATGCTCTACTACCTTCCAACTAGAAATGAGATCGTCTTCCCGCTGGC	1740
QY	1980	ATCTCTGACAGGCCCCCTTTCTATATGCCCGCAACAACCCCAAGGCCCTGAACTTTGTGTGCAATC	2039
Db	1741	ATCTCTGACAGGCCCCCTTTCTATATGCCCGCAACAACCCCAAGGCCCTGAACTTTGTGTGCAATC	1800
QY	2040	GATGTGTGATGTGGGCGCATGAGTTGACGCAATGCTTTTGTATGACCAAGGGCGCGAATATGAC	2099
Db	1801	GATGTGTGATGTGGGCGCATGAGTTGACGCAATGCTTTTGTATGACCAAGGGCGCGAATATGAC	1860
QY	2100	AAAGAGGGGAACTTGCGGCGCCTGTGTGTGCGAGATGATCCCTGTGACGCCCTTCCGGAACAC	2159
Db	1861	AAAGAGGGGAACTTGCGGCGCCTGTGTGTGCGAGATGATCCCTGTGACGCCCTTCCGGAACAC	1920
QY	2160	ACGGCTTGCATGTAGAGGAACAGTAACTAAATACCAAGGTCAATGGGAGAGGCTCAACGGC	2219
Db	1921	ACGGCTTGCATGTAGAGGAACAGTAACTAAATACCAAGGTCAATGGGAGAGGCTCAACGGC	1980
QY	2220	CGCCAGAGCGCTGGGGGAGAAACATTTGCTGACAAACGGGGGCTGGAAGGCTGCTCAATATGCT	2279
Db	1981	CGCCAGAGCGCTGGGGGAGAAACATTTGCTGACAAACGGGGGCTGGAAGGCTGCTCAATATGCT	2040
QY	2280	TACAAAGCATGGCTGAGAAAGCATGGGGAGAGCAACTTGCCAGCCGTGTGGGCTCAAC	2339

Db	2041	TACAAAGCATGGCTGAGAAAGCATGGGAGAGAGAGAACTGGCCAGCCGTGGGCTACCC	2100
Qy	2340	AACCAACGACTCTTCTTGTTGGGAAATTGGCCAGGTGTGATGCTGGATCCGACACAGAG	2399
Db	2101	AAACCAACGACTCTTCTTGTTGGAAATTGGCCAGGTGTGATGCTGGATCCGACACAGAG	2160
Qy	2400	AGCTCTCAGAGGGGGCTGTGTGATCCGACCCCAAGCCCTTCCCGTGTCTGGC	2459
Db	2161	AGCTCTCAGAGGGGGCTGTGTGATCCGACCCCAAGCCCTTCCCGTGTCTGGC	2220
Qy	2460	ACTCTCTCCAACTCCCGGACTTCTGTGGGACTTGGGCTGCCCTGTCCGCTCCCATG	2519
Db	2221	ACTCTCTCCAACTCCCGGACTTCTGTGGGACTTGGGCTGCCCTGTCCGCTCCCATG	2280
Qy	2520	AACCCAGGGGACGCTGTGTGAGGTGTGGTAGACCTGATTCAGGGGAGAAATGCCAGCTGT	2579
Db	2281	AAACCAAGGGGACGCTGTGTGAGGTGTGGTAGACCTGATTCAGGGGAGAAATGCCAGCTGT	2340
Qy	2580	CACCAAGACTTGGGGACGCTCTCTGACAAAGCTGTTGCTTGTGGTTGGAGAGACAA	2639
Db	2341	CACCAAGACTTGGGGACGCTCTCTGACAAAGCTGTTGCTTGTGGTTGGAGAGACAA	2400
Qy	2640	ATGCAAGCTGGGGCTGGGCTTAGTCCCTCCGCCACAGGTGACATGAGTACAGACCTCC	2699
Db	2401	ATGCAAGCTGGGGCTGGGCTTAGTCCCTCCGCCACAGGTGACATGAGTACAGACCTCC	2460
Qy	2700	TCAATTCACCAATTTGTCCTCTGTTTGGGGGTGCCCTGCTTCAGACAGCCCCCACC	2759
Db	2461	TCAATTCACCAATTTGTCCTCTGTTTGGGGGTGCCCTGCTTCAGACAGCCCCCACC	2520
Qy	2760	ATTCACTGTGATCAATCTTTCCGTGTACCTCTGATCCCTGTGAAGAAGTCTGGTGGAGGCTAG	2819
Db	2521	ATTCACTGTGATCAATCTTTCCGTGTACCTCTGATCCCTGTGAAGAAGTCTGGTGGAGGCTAG	2580
Qy	2820	TTCCCATTTGGAAGAAGTCTGCC	2841
Db	2581	TTCCCATTTGGAAGAAGTCTGCC	2602
RESULT 4			
ID	AACT8592	standard; cdNA; 2602 BP.	
XX	AACT8592;		
DT	08-FEB-2001	(first entry)	
DE	Human PR0403	nucleotide sequence SEQ ID NO:525.	
XX	Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;		
KW	expressed sequence tag; detection; cancer; ss.		
OS	Homo sapiens.		
PN	WO200053756-A2.		
PD	14-SEP-2000.		
XX	18-FEB-2000; 2000WO-US004341.		
XX	08-MAR-1999; 99WO-US005028.		
PR	12-MAR-1999; 99US-0123957P.		
PR	29-MAR-1999; 99US-0126773P.		
PR	21-APR-1999; 99US-0130232P.		
PR	28-APR-1999; 99US-0131445P.		
PR	14-MAY-1999; 99US-0134287P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	29-OCT-1999; 99US-0162506P.		
PR	30-NOV-1999; 99WO-US028313.		
PR	02-DEC-1999; 99WO-US028551.		
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OY	1920	CCCCGAGACGAGGAATGCGCTACCTACCTTCCACTAGAAATGATGCTCTTCCCGCTGGC	1979
Db	1681	CCCCGAGACGAGGAATGCGCTACCTACCTTCCACTAGAAATGATGCTCTTCCCGCTGGC	1740
OY	1980	ATCTCGACGGGCCCCCTTCTATGCCCCGCGACCAACCCTCAAGGCGCTTGAATTCCGATGCAATC	2039
Db	1741	ATCTCGACGGGCCCCCTTCTATGCCCCGCGACCAACCCTCAAGGCGCTTGAATTCCGATGCAATC	1800
OY	2040	GGTGTGTCATAGGCGCCATGAGTTGACGCAATGCTTTGATGACCAAGGCGCGAGTATGAC	2099
Db	1801	GGTGTGTCATAGGCGCCATGAGTTGACGCAATGCTTTGATGACCAAGGCGCGAGTATGAC	1866
OY	2100	AAAGGAGGGGAACCTGCGGCGCCCTGGGTGGGAGAAATGATGCTCCCTGCGAGCCCTTCCGAAACAC	2158
Db	1861	AAAGGAGGGGAACCTGCGGCGCCCTGGGTGGGAGAAATGATGCTCCCTGCGAGCCCTTCCGAAACAC	1920
OY	2160	ACGCGCTTCATAGAGGAACAAGTACAATCAATACAGAGTCAATGAGGAGAGGCTCAACGGC	2219
Db	1921	ACGCGCTTCATAGAGGAACAAGTACAATCAATACAGAGTCAATGAGGAGAGGCTCAACGGC	1980
OY	2220	CGCCGACGCTTGGGGGAGAACATTGCTGACCAACGGGGGGCTGAAGGCTGCTCAATGCT	2279
Db	1981	CGCCGACGCTTGGGGGAGAACATTGCTGACCAACGGGGGGCTGAAGGCTGCTCAATGCT	2040
OY	2280	TACCAAGCATGCTGAGAAAGCATGAGGAGAGACGACATCTCCAGCCGTGGGGCTCAC	2339
Db	2041	TACCAAGCATGCTGAGAAAGCATGAGGAGAGACGACATCTCCAGCCGTGGGGCTCAC	2100
OY	2340	AACCAACGAGCTCTTCTGTGGGGAATTTGCTCCAGGGTGTGCTCGGTCCGACACCAAG	2399
Db	2101	AACCAACGAGCTCTTCTGTGGGGAATTTGCTCCAGGGTGTGCTCGGTCCGACACCAAG	2160
OY	2400	AGCTTCACGAGGGGCTGTGACCGACCCCAACGCGCTGCGCTTCCGCGTGTGGG	2459
Db	2161	AGCTTCACGAGGGGCTGTGACCGACCCCAACGCGCTGCGCTTCCGCGTGTGGG	2220
OY	2460	ACTCTCTCCAACTCCCGTGACCTTCTGTGGGCACTTCCGCTGCTGTGGCTCCCCATG	2519
Db	2221	ACTCTCTCCAACTCCCGTGACCTTCTGTGGGCACTTCCGCTGCTGTGGCTCCCCATG	2280
OY	2520	AACCCAGGGGAGCTGTGTGAGGTGTGTGAGACCTGGAATCAAGGGGAGAAATGCCAGAGCT	2579
Db	2281	AACCCAGGGGAGCTGTGTGAGGTGTGTGAGACCTGGAATCAAGGGGAGAAATGCCAGAGCT	2340
OY	2580	CACCAAGACTGGGGCAGCTCTCTGACAAAGCTGTTGCTTGGGTTGGAGGAAGCA	2639
Db	2341	CACCAAGACTGGGGGAGCTCTCTGACAAAGCTGTTGCTTGGGTTGGAGGAAGCA	2400
OY	2640	ATGCAAGCTGGGAGTGTGATGCTTGTAGTCCCTCCCCCAACAGGTACATGATACAGACCTCC	2699
Db	2401	ATGCAAGCTGGGAGTGTGATGCTTGTAGTCCCTCCCCCAACAGGTACATGATACAGACCTCC	2460
OY	2700	TCAATTCACCAATGTGCTCTGCTCTTGTGGGGGTGCCCTGCTCCAGAGAGCCCCCAAC	2759
Db	2461	TCAATTCACCAATGTGCTCTGCTCTTGTGGGGGTGCCCTGCTCCAGAGAGCCCCCAAC	2520
OY	2760	ATTCACTGTGACATCTTCCGCTGTCAACCGTCTTGAAGAGGTCTGGGTGGGAGGCGAG	2819
Db	2521	ATTCACTGTGACATCTTCCGCTGTGTCAACCGTCTTGAAGAGGTCTGGGTGGGAGGCGAG	2580
OY	2820	TTCCCATAGGAAGAGTCTGCC 2841	
Db	2581	TTCCCATAGGAAGAGTCTGCC 2602	
RESULT 5			
AAS46134			
ID AAS46134 standard; cDNA; 2602 BP.			
XX AAS46134;			
XX			
XX 18-DEC-2001 (first entry)			

DE Human DNA encoding PRO polypeptide sequence #210.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;

KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;

KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;

KW PCR primer.

OS Homo sapiens.

PN WO200168848-A2.

XX 20-SEP-2001.

PD 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

PP 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005844.

XX 03-MAR-2000; 2000US-0187202.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 14-MAR-2000; 2000US-0189328P.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008433.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

XX 11-APR-2000; 2000US-0195975P.

XX 11-APR-2000; 2000US-0196000P.

XX 11-APR-2000; 2000US-0196187P.

XX 11-APR-2000; 2000US-0196690P.

XX 11-APR-2000; 2000US-0196820P.

XX 18-APR-2000; 2000US-0198121P.

XX 18-APR-2000; 2000US-0198585P.

XX 25-APR-2000; 2000US-0199397P.

XX 25-APR-2000; 2000US-0199550P.

XX 25-APR-2000; 2000US-0199654P.

XX 03-MAY-2000; 2000US-0201516P.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 22-AUG-2000; 2000US-0064484P.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000WO-US034956.

PA (GENTH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PU, Gurney AL;

PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-602746/68.

DR P-PSDB; AAU29233.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the

PT presence of tumors, such as prostate and breast tumors, in mammals and to

PT screen for modulators of the compounds.

XX Claim 2; Fig 419; 774pp; English.

XX Sequences AAS45923-AAS46231 represent DNA molecules encoding and PCR

CC primers for PRO polypeptides of the invention. The sequences of the

CC invention can be used to detect the presence of a tumour in a mammal by





Db 1981 CGCAGACGCTGGGGAGAAATTACTGACACGGGGGGCTGAAGGCTGCTCAATGCT 2040  
QY 2280 TACAAAGCATGGCTGAGAAAGCATGGGAGAGACAGCAATTGCCAGCCGTGGGGCTCACC 2339  
Db 2041 TACAAAGCATGGCTGAGAAAGCATGGGAGAGACAGCAATTGCCAGCCGTGGGGCTCACC 2100  
QY 2340 AACCAACAGCTCTTCTTCGCGGATTTGCCAGGTGGTGTCTGGTCCGACACAGAG 2399  
Db 2101 AACCAACAGCTCTTCTTCGCGGATTTGCCAGGTGGTGTCTGGTCCGACACAGAG 2160  
QY 2400 AGCTCTCAGAGGGGGCTGTGACCAACCCCAAGCCCTGCCCTTCGCGGTGAGGC 2459  
Db 2161 AGCTCTCAGAGGGGGCTGTGACCAACCCCAAGCCCTGCCCTTCGCGGTGAGGC 2220  
QY 2460 ACTCTCTCCAACTCCCGTGACTTCTCCGCGCACTTGAGCTGCTGCTGCTCCCATG 2519  
Db 2221 ACTCTCTCCAACTCCCGTGACTTCTCCGCGCACTTGAGCTGCTGCTGCTCCCATG 2280  
QY 2520 AACCCAGGGAGCTGTGTGAGGTGGTGAACCTGATCAGGGAGAAATGCCAGCTGT 2579  
Db 2281 AACCCAGGGAGCTGTGTGAGGTGGTGAACCTGATCAGGGAGAAATGCCAGCTGT 2340  
QY 2580 CACCAAGCTGGGGAGCTCTCCTGACAAAGCTGTTGCTCTTGGGTTGGAGAAACAA 2639  
Db 2341 CACCAAGCTGGGGAGCTCTCCTGACAAAGCTGTTGCTCTTGGGTTGGAGAAACAA 2400  
QY 2640 ATGCAAGCTGGGGTGGGTCTAGTCCCTCCCGCCAGAGGTGACATGATACAGACTTC 2699  
Db 2401 ATGCAAGCTGGGGTGGGTCTAGTCCCTCCCGCCAGAGGTGACATGATACAGACTTC 2460  
QY 2700 TCATCACCACATTTGCTCTGCTTGGGGGGTGGCCCTGCCAGCAGAGCCCAACC 2759  
Db 2461 TCATCACCACATTTGCTCTGCTTGGGGGGTGGCCCTGCCAGCAGAGCCCAACC 2520  
QY 2760 ATTCACCTGTGACATCTTTCGCTGACCCCTGAGAGAGGTCTGAGTGGAGGCCAG 2819  
Db 2521 ATTCACCTGTGACATCTTTCGCTGACCCCTGAGAGAGGTCTGAGTGGAGGCCAG 2580  
QY 2820 TTCCCATAGGAAGAGTCTGCC 2841  
Db 2581 TTCCCATAGGAAGAGTCTGCC 2602

RESULT 6  
ABX78737  
ID ABX78737 standard; cDNA; 2602 BP.  
XX  
AC ABX78737;  
XX  
DT 15-APR-2003 (first entry)  
XX  
DE Human PRO polynucleotide #210.  
XX  
KW Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;  
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;  
KW antibody-dependent enzyme mediated prodruug therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027272-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176492.  
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PR 24-OCT-1997; 97US-0063120P.  
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PR 07-OCT-1998; 98US-00168978.

Query Match 72.9%; Score 2461.2; DB 7; Length 2602;  
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QY 420 ACGCACTGAGCTGTCTTACAGAGTGCCTCTTACTCTGCTGCTGCTTCTGGCC 479  
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QY 480 TGCCTTGTGGCCTTAGGGCTCCAGTACCAAGAGACCATCCACAGCACCTGCTTACA 539  
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XX 13-FEB-2003.  
PD 26-JUN-2002; 2002US-00183012.  
PF XX  
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DB 301 GAGGCTGATTCGAGTGGCTGAAAAATCTGAGTCCCTGAGCCGAGGGGTGAGCCCC 360  
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QY	720	CACCTGCTTGAAGAAACAC	CACTTCAACCTCCAGAGTGAAGCTGACAGAAACA	779	
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QY	1080	TATCTGGAATTA	CTGAGAGAACTGGGGAGTGGTGGTGGGGGGGGCCCACTCCACGAG	1139	
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QY	1920	CCCCAGACAGTAATGCTACTACCTTCCAACTAAGAAATGATCGCTTCCCGCTGGC	1979
Db	1681	CCCCAGACAGTAATGCTACTACTACCTTCCAACTAAGAAATGATCGCTTCCCGCTGGC	1740
QY	1980	ATCTGACAGGCCCCCTTCTATGCCCCGAGACCAACCCAGAGCCCTGAACTTCGATGAC	2039
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QY	2040	GGTGTGTCATGAGCCCATGAGTTGACGATGCTTTGATGACAAAGGCGGAGTATGAC	2099
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QY	2100	AAAGAAGGAAACCTGCGGCTCTGCTGTCAGAAATGATCCTGAGAGCTTCCGAAACAC	2159
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antithratic; vulnerary; gene therapy; gene; ss.  
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KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;



Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 420 ACCGACGTGGAGCTGTGCTTAGAGAGGCTCTCTACTGTGGCTGGACGCTTTCTGGG 479  
DB 181 ACCGACGTGGAGCTGTGCTTAGAGAGGCTCTCTACTGTGGCTGGACGCTTTCTGGG 240  
QY 480 TGGCTTGTGGCCCTAGGGGATCCAGTACACAGAGACCCATCCACAGACCTGCTTACA 539  
DB 241 TGGCTTGTGGCCCTAGGGGATCCAGTACACAGAGACCCATCCACAGACCTGCTTACA 300  
QY 540 GAGGCTTGCATTTGAGTGTGGGAAAAATCTTGAAGTCTGGAACGAGGGGTGAGCC 599  
DB 301 GAGGCTTGCATTTGAGTGTGGGAAAAATCTTGAAGTCTGGAACGAGGGGTGAGCC 360  
QY 600 TGTGAGGACTTTTACAGGTTCTCTGTGGGGCTGGAATTCGAGAGAAACCCCTGCCGAT 659  
DB 361 TGTGAGGACTTTTACAGGTTCTCTGTGGGGCTGGAATTCGAGAGAAACCCCTGCCGAT 420  
QY 660 GGGCGTTCTGCTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGGCTATGTAAG 719  
DB 421 GGGCGTTCTGCTGGAACACCTTCAACAGCCTCTGGGACCAAAACAGGCTATGTAAG 480  
QY 720 CACCTGCTTGAACACACACCTTCAACCTCAGCAGTGAAGCTGAGAGAGAGACAGCC 779  
DB 481 CACCTGCTTGAACACACACCTTCAACCTCAGCAGTGAAGCTGAGAGAGAGACAGCC 540  
QY 780 TTCTACCTATCTTGCCCTACAGGTGAGCGCATTGAGAGGCTGGGAGCCAGCCACTGAGA 839  
DB 541 TTCTACCTATCTTGCCCTACAGGTGAGCGCATTGAGAGGCTGGGAGCCAGCCACTGAGA 600  
QY 840 GACCTCATTTGAGAGATTTGGTGTGGACATTACGGGGCCCTGGGACAGAGCAATTT 899  
DB 601 GACCTCATTTGAGAGATTTGGTGTGGACATTACGGGGCCCTGGGACAGAGCAATTT 660  
QY 900 ATGGAAGTGTGGAAGGACGAGAGGAGCCTACAGGGCCACCCATTTCTACCTGTAC 959  
DB 661 ATGGAAGTGTGGAAGGACGAGAGGAGCCTACAGGGCCACCCATTTCTACCTGTAC 720  
QY 960 ATCAGTGCAGACTCTAAGAGTTCCACAGCAATGTTATCCAGGTGAGCACTGCGGCTC 1019  
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QY 1080 TATCTGAGATTAATGAGAGAACTGGGAGTCTGCTGGGTGGGGCCACCTTCAAGAG 1139  
DB 841 TATCTGAGATTAATGAGAGAACTGGGAGTCTGCTGGGTGGGGCCACCTTCAAGAG 900  
QY 1140 GAGCAGATGACAGAGGTGCTGAGTTGAGATACAGTGGCCAACTACAGTGGCCAG 1199  
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QY 2340 AACCAACAGCTCTTCTGCTGAGATTTGCGCAGGTGTGTGCTCGTCCGCAACAGAG 2399  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
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DB 181 ACGCAGCTGAGCTGCTTTAGCAGGTGCTCTTACTGCTGAGCTGCTGCTTTCTGAGC 240  
QY 480 TGCCTTGTGGCCCTTGGGCTCAGTACCAAGAACCCATCCACAGCACTGCTTTACA 539  
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DE  
XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;  
KW chondrocyte differentiation; tumour necrosis factor-alpha release; ss;  
KW affinity purification; gene.  
XX  
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XX  
XX US2003036147-A1.  
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XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-00187741.  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY 480 TGCCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGGCTTGGAGG 539  
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QY 600 TGTGAGAGCTTGTACAGATTTCTTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGG 659  
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QY 660 GGGCGTTCTGCTGGAACACTTCAACAGCTCTGGGACCAAAACAGGCGCATCTGAG 719  
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DB 481 CACCTGCTTGAAGACACACCTTCACTTCAGAGTGAAGCTTGAAGACACAGGCG 540  
QY 780 TTTCTACTATCTTGGCTTACAGGTGAGGCGCATTTGAGAGCTGAGGCGCATCTGAG 839  
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Q 1080 TATCTGATTAATCAATGAGAACTGGGATGCTGCTGGTGGGCGGCCCATCTTCACAGAG 1139  
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D 2221 ACTCTCTCAACTCCCGTGAATCTTCTGCGGCACTTGGGCTGCGCTGCCCTCCCATG 2280  
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KW liver; drug screening; transgenic animal; genetic analysis;  
KW antitartaric; vulnerary; gene therapy; gene; ss.  
XX Homo sapiens.  
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Query Match 72.9%; Score 2461.2; DB 7; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0; Mismatches 13; Indels 0; Gaps 0;

Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 241 TGGCTTGGGCGCTAGGAGGCTCAGTACCAAGAGAGCCATCCAGACCTGCGCTTACA 300  
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QY 660 GGGGCTTCTGCTGAGAAACACTTCAACAGGCTGAGGAGCAAAACAGGCTATAGAG 719  
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QY	2881	GCTGCGCGTGCCTGGCCCACTGTACCCAGAGGCTCTGAGGCTGAGGAGTACTCCCTGACATTCT	2940
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QY	2941	CCCCAGGCTCACTCAGTGCAGACTTAAAGGGTGTGACTCAGCTCTGTCTTGGCTCAACCTTAC	3000
Db	2941	CCCCAGGCTCACTCAGTGCAGACTTAAAGGGTGTGACTCAGCTCTGTCTTGGCTCAACCTTAC	3000
QY	3001	GGGCTACCCCACTCACTCAGTGTGCTCTTGTGCGCATCTGTCGCCAGTGTGCTCTGAC	3060
Db	3001	GGGCTACCCCACTCACTCAGTGTGCTCTTGTGCGCATCTGTCGCCAGTGTGCTCTGAC	3060
QY	3061	TTCACTGACAGTCTCTTGTGAGAGCCAAAGGGCCCTGTAAAGCTCTCTGCTGCCACTGT	3120
Db	3061	TTCACTGACAGTCTCTTGTGAGAGCCAAAGGGCCCTGTAAAGCTCTCTGCTGCCACTGT	3120
QY	3121	TTCCCTGGGCTGAGGGGGAAGTGCATATGTGTAGCGGATCTGGTTCTGTGTCTTAAG	3180
Db	3121	TTCCCTGGGCTGAGGGGGAAGTGCATATGTGTAGCGGATCTGGTTCTGTGTCTTAAG	3180
QY	3181	GCAACAAGCTTAGCAAAATGATTTGCTTCCTCTGACAAAGCAAGAGAAAGACATAGAGAG	3240
Db	3181	GCAACAAGCTTAGCAAAATGATTTGCTTCCTCTGACAAAGCAAGAGAAAGACATAGAGAG	3240
QY	3241	GGAAAAAGAAAGACAGAGTTTATTTTTCACAAAAAGAGGTGGAGGGGTGTGTCTTGCC	3300
Db	3241	GGAAAAAGAAAGACAGAGTTTATTTTTCACAAAAAGAGGTGGAGGGGTGTGTCTTGCC	3300
QY	3301	CCTTATAGAGACTGTGTGCATTAACACAGACTGCATCCGTCAAAAAA	3360
Db	3301	CCTTATAGAGACTGTGTGCATTAACACAGACTGCATCCGTCAAAAAA	3360
QY	3361	AAAAAAAAAAAAAAAA 3377	
Db	3361	AAAAAAAAAAAAAAAA 3377	

RESULT 2  
US-10-453-764-1  
: Sequence 1, Application US/10453764

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: Publication No. US2003023044A1
: GENERAL INFORMATION:
: APPLICANT: White, David
: TITLE OF INVENTION: USE FOR ENDOTHELIN CONVERTING ENZYME 2
: TITLE OF INVENTION: (ECC-2) IN THE DIAGNOSIS AND TREATMENT OF METABOLIC
: TITLE OF INVENTION: DISORDERS
: FILE REFERENCE: MP102-266P1RM
: CURRENT APPLICATION NUMBER: US/10/453,764
: CURRENT FILING DATE: 2003-06-03
: PRIOR APPLICATION NUMBER: 60/386,333
: PRIOR FILING DATE: 2002-06-05
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3138
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (49)...(2346)
US-10-453-764-1

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DB	1 CGGGCCAGCTGCGCGGAGCCCTGATATCA	CGGCCTGGCCCGATCTCACCATGAA	CGTCCG	60	
QY	126 CTGACGAGAGCTGGGAGCTGGGACAGCA	CAATGTTGAGTACAAACGGGCCACGCTTCGGGAT	185		
DB	61 CTGACGAGAGCTGGGAGCTGGGACAGCA	CAATGTTGAGTACAAACGGGCCACGCTTCGGGAT	120		
QY	186 GAAAGACGACCCCGAGACCCCGCTGAG	GGGGCGGCGCTCCCGGACGACATGAGAGTGGCG	245		
DB	121 GAAAGACGACCCCGAGACCCCGCTGAG	GGGGCGGCGCTCCCGGACGACATGAG	173		
QY	246 AAGGGAGCTTCCCTTTCTCACCA	GGGCCCGACGCTTGACACACCCAG	305		
DB	174 -----	-----	173		
QY	306 AGCTCTGGGCTGTTCTGGAGGGTCA	CTGCCCCACCTCCGCTCATCTTGGGCTTGC	365		
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QY	426 CTGAGAGCTGCTTAGACAGGTGCTCTCTA	CTGCTGGCTGCATGCTTCTTGGGCTGCCTT	485		
DB	223 CTGAGAGCTGCTTAGACAGGTGCTCTCTA	CTGCTGGCTGCATGCTTCTTGGGCTGCCTT	282		
QY	486 GTGGCCCTAGGGGTTCCAGTACACAGAG	ACCATCCACAGCAGCTTGCTTACAGAGCC	545		
DB	283 GTGGCCCTAGGGGTTCCAGTACACAGAG	ACCATCCACAGCAGCTTGCTTACAGAGCC	342		
QY	546 TGCATTTGAGAGTGGGTTGAAAAATCT	CTGAGTCCCTGACCGAGGGGGTGAAGCCCTGTAG	605		
DB	343 TGCATTTGAGAGTGGGTTGAAAAATCT	CTGAGTCCCTGACCGAGGGGGTGAAGCCCTGTAG	402		
QY	606 GACTTTTACAGATCTCTCTGTGGGGGCT	GTGATTTCCAGAGAACCCCTTGCCGATAGGGCGT	665		
DB	403 GACTTTTACAGATCTCTCTGTGGGGGCT	GTGATTTCCAGAGAACCCCTTGCCGATAGGGCGT	462		
QY	666 TCTGCTGGAAACATTTCAAACAGCT	CTGGGACCAAAACCAAGGCTATCTGAGCAGCTG	725		
DB	463 TCTGCTGGAAACATTTCAAACAGCT	CTGGGACCAAAACCAAGGCTATCTGAGCAGCTG	522		
QY	726 CTTGAAAAACACACTTCAACTCCAGAG	AGTGAAGTGAAGACAGACAGCGCTTCTAC	785		
DB	523 CTTGAAAAACACACTTCAACTCCAGAG	AGTGAAGTGAAGACAGACAGCGCTTCTAC	582		

QY 786 CTATCTTGGCTAGAGGTGAGCGCATTTGAGAGCTGGAGGCCAGGCACTGAGAGCACTC 845  
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Db 703 GTGTTGAAGGCACTGAGGAGCACTTACAGGGGCCACCCCATTTCTTCACTGCTTACATCAGT 762  
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Db 763 GCTGACTTAAAGTTCACACAGCAATGTTATCCAGGTGAGCAAGTCTGGGCTCTTCTG 822  
QY 1026 CCTCTCGGAGTAACTTAAACAGAACTGCCAATGAGAAAGTGTCTCACTGCTTATCTG 1085  
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QY 1806 GAAATTTCTGAAGATTTCTTCTTCAAAACATGTTGAATTTGTAACAATTTCTGCGCAG 1865  
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Db 1603 GAAATTTCTGAAGATTTCTTCTTCAAAACATGTTGAATTTGTAACAATTTCTGCGCAG 1662

QY 1866 GTTATGCTGACCAAGCTCCGCAAGCTCCGACCGAGACAGTGGAGATGACCCCGCAG 1925  
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QY 420 AGGCACTGAGAGCTGCTTTAGCAGGTGCTCTTACTGCTGGCTGCACTGCTTGGGC 479  
DB 181 AGCAGAGCTGAGAGCTGCTTTAGCAGGTGCTCTTACTGCTGGCTGCACTGCTTGGGC 240

QY 480 TGCTTGTGGCCCTTAGGGGTCCAGTACACAGAGACCATCCACAGCACTGCTTACA 539  
DB 241 TGCTTGTGGCCCTTAGGGGTCCAGTACACAGAGACCATCCACAGCACTGCTTACA 300

QY 540 GAGGCTGCAATTCAGAGTGTGAGAAATCTCTGAGTCTCTGAGCCGAGGGGTGAGCCC 599  
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QY 600 TGTGAGAGCTTTTACCAAGTTTCCTGTGGGGCTGATTCGAGAGAACCCCTGCCCAT 659  
DB 361 TGTGAGAGCTTTTACCAAGTTTCCTGTGGGGCTGATTCGAGAGAACCCCTGCCCAT 420

QY 660 GGGCGTTCTGCTGAGAACACTTCAACAGCTCTGAGACCAAAACAGGCCATACTGAG 719  
DB 421 GGGCGTTCTGCTGAGAACACTTCAACAGCTCTGAGACCAAAACAGGCCATACTGAG 480

QY 720 CACTGCTTGAAGAACCACTTCACTCAGAGTGAAGCTGAGCAAGAACACAGGCC 779  
DB 481 CACTGCTTGAAGAACCACTTCACTCAGAGTGAAGCTGAGCAAGAACACAGGCC 540

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QY 1200 GACCAAGCGGCGAGCAGAGAGAAATCTTACCAAGATGAGCATTTGAGAGTGCAGGCT 1259



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23	PRIOR APPLICATION NUMBER: 60/082804
24	PRIOR FILING DATE: 1998-04-22
25	PRIOR APPLICATION NUMBER: 60/082700
26	PRIOR FILING DATE: 1998-04-22
27	PRIOR APPLICATION NUMBER: 60/082797
28	PRIOR FILING DATE: 1998-04-22
29	PRIOR APPLICATION NUMBER: 60/082796
30	PRIOR FILING DATE: 1998-04-23
31	PRIOR APPLICATION NUMBER: 60/083336
32	PRIOR FILING DATE: 1998-04-27
33	PRIOR APPLICATION NUMBER: 60/083322
34	PRIOR FILING DATE: 1998-04-28
35	PRIOR APPLICATION NUMBER: 60/083392
36	PRIOR FILING DATE: 1998-04-29
37	PRIOR APPLICATION NUMBER: 60/083455
38	PRIOR FILING DATE: 1998-04-29
39	PRIOR APPLICATION NUMBER: 60/083456
40	PRIOR FILING DATE: 1998-04-29
41	PRIOR APPLICATION NUMBER: 60/083499
42	PRIOR FILING DATE: 1998-04-29
43	PRIOR APPLICATION NUMBER: 60/083545
44	PRIOR FILING DATE: 1998-04-29
45	PRIOR APPLICATION NUMBER: 60/083554
46	PRIOR FILING DATE: 1998-04-29
47	PRIOR APPLICATION NUMBER: 60/083558
48	PRIOR FILING DATE: 1998-04-29
49	PRIOR APPLICATION NUMBER: 60/083559
50	PRIOR FILING DATE: 1998-04-29
51	PRIOR APPLICATION NUMBER: 60/083500
52	PRIOR FILING DATE: 1998-04-29
53	PRIOR APPLICATION NUMBER: 60/083742
54	PRIOR FILING DATE: 1998-04-30
55	PRIOR APPLICATION NUMBER: 60/084366
56	PRIOR FILING DATE: 1998-05-05
57	PRIOR APPLICATION NUMBER: 60/084414
58	PRIOR FILING DATE: 1998-05-06
59	PRIOR APPLICATION NUMBER: 60/084411
60	PRIOR FILING DATE: 1998-05-06
61	PRIOR APPLICATION NUMBER: 60/084637
62	PRIOR FILING DATE: 1998-05-07
63	PRIOR APPLICATION NUMBER: 60/084639
64	PRIOR FILING DATE: 1998-05-07
65	PRIOR APPLICATION NUMBER: 60/084640
66	PRIOR FILING DATE: 1998-05-07
67	PRIOR APPLICATION NUMBER: 60/084598
68	PRIOR FILING DATE: 1998-05-07
69	PRIOR APPLICATION NUMBER: 60/084600
70	PRIOR FILING DATE: 1998-05-07
71	PRIOR APPLICATION NUMBER: 60/084622
72	PRIOR FILING DATE: 1998-05-07
73	PRIOR APPLICATION NUMBER: 60/084633
74	PRIOR FILING DATE: 1998-05-07







PRIOR FILING DATE:	1986-04-01
PRIOR APPLICATION NUMBER:	60/080333
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/080334
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/081070
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PRIOR APPLICATION NUMBER:	60/081203
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PRIOR FILING DATE:	1998-04-15
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323-3
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085669-9
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579-9
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580-0
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573-3
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704-4
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085637-7

Query Match	72.9%	Score 2461.2	DB 9	Length 2602
Best Local Similarity	99.5%	Pred. No. 0		
Matches 2469; Conservative	0	Mismatches 13	Indels 0	Gaps 0

Qy	360	CTCTGCTCATTAGACATCATGGTGGGATTTCCAGAAAGGGGACACAGACAGCTGTATAGCTCACGC	41.9
Db	121	CTGGAGAGCTGGACGACACCTGGGATTTCCAGAAAGGGGACACAGACAGCTGTATAGCTCACGC	18.0
Qy	420	ACGCAGCTGGAGCTGCTCTTAAGCAGTGCCTCTCACTGTGCTGCACTGTCTTTGAGC	47.9
Db	181	ACGCAGCTGGAGCTGCTCTTAAGCAGTGCCTCTCACTGTGCTGCACTGTCTTTGAGC	24.0
Qy	480	TGCTTTTGAGGCTTGAAGGGGTCCAGTACACAGACAGCCATCCACACACACTGCTTACA	53.9
Db	241	TGCTTTTGAGGCTTGAAGGGGTCCAGTACACAGACAGCCATCCACACAGACTGCTTACA	30.0
Qy	540	GAGGCTGTGATTCGAGTGGCTGGAAAAATCCTGAGTCCCTGACCCGAGGGGTGAGCCC	59.9
Db	301	GAGGCTGTGATTCGAGTGGCTGGAAAAATCCTGAGTCCCTGACCCGAGGGGTGAGCCC	36.0
Qy	600	TGTGAGAGATTTTACCAATTCCTCTGTGGGGGGGCTGAGTTGAGAGAAACCCCTGCCGAT	65.9
Db	361	TGTGAGAGATTTTACCAATTCCTCTGTGGGGGGGCTGAGTTGAGAGAAACCCCTGCCGAT	42.0
Qy	660	GGGCGTTCTCGCTGGAGACCTTCACACAGCCTCTGGGACCAAAACAGAGCATCTAGTAG	71.9
Db	421	GGGCGTTCTCGCTGGAGACCTTCACACAGCCTCTGGGACCAAAACAGAGCATCTAGTAG	48.0
Qy	720	CACCTGCTTGA AAAACACACCTTCACATCTCCAGCAGTGAAGCTGAGCGAAGACACAGCCG	77.9
Db	481	CACCTGCTTGA AAAACACACCTTCACATCTCCAGCAGTGAAGCTGAGCGAAGACACAGCCG	54.0
Qy	780	TTCTACCTATCTTGGCTACAGGTGAGGCAATTGAGAGCTGGGAGCCACGCACTGAGA	83.9
Db	541	TTCTACCTATCTTGGCTACAGGTGAGGCAATTGAGAGCTGGGAGCCACGCACTGAGA	60.0
Qy	840	GACCTCATTTGAGAGATTTGTGTGTTGGAACATTAACGGGGCCCTGGGACACGAGCAACTTT	89.9
Db	601	GACCTCATTTGAGAGATTTGTGTGTTGGAACATTAACGGGGCCCTGGGACACGAGCAACTTT	66.0

QY 900 ATGAGGTGTTGAAGCAATGACAGGAGCACTACAGGGGCAACCCATCTTCAACGCTTAC 959  
 DB 661 ATGAGGTGTTGAAGCAATGACAGGAGCACTACAGGGGCAACCCATCTTCAACGCTTAC 720  
 QY 960 ATGAGTCCGACCTTAAGATTCCACAGCAATGTTATCCAGGTGAGCAAGTCTGAGCTC 1019  
 DB 721 ATGAGTCCGACCTTAAGATTCCACAGCAATGTTATCCAGGTGAGCAAGTCTGAGCTC 780  
 QY 1020 TTTCTGCTCTCTGAGGATTACTTAACAGAACTGCAATGAGAAAGTCTCACTGCC 1079  
 DB 781 TTTCTGCTCTCTGAGGATTACTTAACAGAACTGCAATGAGAAAGTCTCACTGCC 840  
 QY 1080 TATCTGATTAACATGAGGAACTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1139  
 DB 841 TATCTGATTAACATGAGGAACTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 900  
 QY 1140 GAGCAGATGACAGAGGTGCTGAGGAGTGAAGATACAGCTGAGCAATCAAGTGCCTCAG 1199  
 DB 901 GAGCAGATGACAGAGGTGCTGAGGAGTGAAGATACAGCTGAGCAATCAAGTGCCTCAG 960  
 QY 1200 GACCAAGGCGGCGACAGAGAGAGATCTACCAAGATGACATTTGAGCTGAGGCT 1259  
 DB 961 GACCAAGGCGGCGACAGAGAGAGATCTACCAAGATGACATTTGAGCTGAGGCT 1020  
 QY 1260 CTGGCGGCTCCATGAGCTGAGTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1319  
 DB 1021 CTGGCGGCTCCATGAGCTGAGTCTGAGTCTGCTGCTTCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1320 AGTGAATCTGAGCTGAGTCTGAGTATGAGATGAGATTAATTTGAGAGAGTGTGAGCTC 1379  
 DB 1081 AGTGAATCTGAGCTGAGTCTGAGTATGAGATGAGATTAATTTGAGAGAGTGTGAGCTC 1140  
 QY 1380 ATCAACCGCACGAGAACCAAGATCTGAACTAATTAATTAATTAATTAATTAATTAAT 1439  
 DB 1141 ATCAACCGCACGAGAACCAAGATCTGAACTAATTAATTAATTAATTAATTAATTAAT 1200  
 QY 1440 ACAACCTCAAGCTGAGCGGACGCTGAGTCTGAGCAAGAGAGAGCTGAGAGAGCTC 1499  
 DB 1201 ACAACCTCAAGCTGAGCGGACGCTGAGTCTGAGCAAGAGAGAGCTGAGAGAGCTC 1260  
 QY 1500 TATGCACTAAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1559  
 DB 1261 TATGCACTAAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1320  
 QY 1560 GCCCTTGGCTTTGCTTTGGGGTCCCTCTTGTGAGGCGCACGTTTGAACCGCAAGCAA 1619  
 DB 1321 GCCCTTGGCTTTGCTTTGGGGTCCCTCTTGTGAGGCGCACGTTTGAACCGCAAGCAA 1380  
 QY 1620 GAAATTCAGAGGGGATGATCAGGAGAAATCCGACCGCATTTGAGAGAGGCGCTGGAGCAG 1679  
 DB 1381 GAAATTCAGAGGGGATGATCAGGAGAAATCCGACCGCATTTGAGAGAGGCGCTGGAGCAG 1440  
 QY 1680 CTGGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1739  
 DB 1441 CTGGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 QY 1740 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1799  
 DB 1501 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 QY 1800 GGGATGAGAAATTTCTGAAGATCTTCTTCTCAAAACAGTTTGAATTTGTAACCTTCTCT 1859  
 DB 1561 GGGATGAGAAATTTCTGAAGATCTTCTTCTCAAAACAGTTTGAATTTGTAACCTTCTCT 1620  
 QY 1860 GCCAAGGTTATGCTGACAGCTCCGACAGCTCCGACGAGAGAGAGAGAGAGAGAGAGAG 1919  
 DB 1621 GCCAAGGTTATGCTGACAGCTCCGACAGCTCCGACGAGAGAGAGAGAGAGAGAGAGAG 1680  
 QY 1920 CCCAAGAGAGTGAATGCTTACCTTCAACATTAAGATGATGCTTCTTCTTCTTCTTCTG 1979  
 DB 1681 CCCAAGAGAGTGAATGCTTACCTTCAACATTAAGATGATGCTTCTTCTTCTTCTTCTG 1740

QY 1980 ATCTGACAGAGGCGGCTTCTATGCTCCGCAACACACCCCAAGGCGCTGAACTTGGTGCATC 2039  
 DB 1741 ATCTGACAGAGGCGGCTTCTATGCTCCGCAACACACCCCAAGGCGCTGAACTTGGTGCATC 1800  
 QY 2040 GGTGTGTATGAGGCGGCTTATGAGTGAAGTCTTGTATGACAAAGGCGGAGATGATC 2099  
 DB 1801 GGTGTGTATGAGGCGGCTTATGAGTGAAGTCTTGTATGACAAAGGCGGAGATGATC 1860  
 QY 2100 AAAAGAGGAGAACTTGGGCGGCTTGTGAGTGAAGTCTTGTGAGTGAAGTCTTGTGAGTGA 2159  
 DB 1861 AAAAGAGGAGAACTTGGGCGGCTTGTGAGTGAAGTCTTGTGAGTGAAGTCTTGTGAGTGA 1920  
 QY 2160 ACAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2219  
 DB 1921 ACAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
 QY 2220 CGCAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2279  
 DB 1981 CGCAGAGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040  
 QY 2280 TACAAAGCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339  
 DB 2041 TACAAAGCATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
 QY 2340 AACCAACAGCTCTTCTTCTGAGGATTTGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2399  
 DB 2101 AACCAACAGCTCTTCTTCTGAGGATTTGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
 QY 2400 AGCTCTCAGAGGAGGCTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459  
 DB 2161 AGCTCTCAGAGGAGGCTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
 QY 2460 ACTCTCTCAACTCCCGGTAATTCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2519  
 DB 2221 ACTCTCTCAACTCCCGGTAATTCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280  
 QY 2520 AACCCAGGAGAGGCTGATGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2579  
 DB 2281 AACCCAGGAGAGGCTGATGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
 QY 2580 CACCAAGCTTGGGAGAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2639  
 DB 2341 CACCAAGCTTGGGAGAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
 QY 2640 ATGCAAGCTGAGGAGGCTGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2699  
 DB 2401 ATGCAAGCTGAGGAGGCTGAGGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460  
 QY 2700 TCAATGACCAATTTGCTCTGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2759  
 DB 2461 TCAATGACCAATTTGCTCTGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520  
 QY 2760 ATTCACTGAGACATCTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2819  
 DB 2521 ATTCACTGAGACATCTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580  
 QY 2820 TTCCCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2841  
 DB 2581 TTCCCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2602

## RESULT 6

US-09-999-832A-525  
 ; Sequence 525, Application US/0999832A  
 ; Publication No. US20020192706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen



PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 9; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 360 CTCGCTCTAGGACTATGATGGGATTCAGAGGGGACAGAGCTGTAGGCTCAGC 419  
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QY 420 ACGAGCTGAGAGCTGATCTTAGCAGGCTCTCTACTGCTGCTGACCTGCTTGGGC 479  
DB 181 ACGAGCTGAGAGCTGATCTTAGCAGGCTCTCTACTGCTGCTGACCTGCTTGGGC 240  
QY 480 TGCTTGTGGCCCTTGGGGGTCAGTACCAAGAGACCCATCCCAAGACCTGCTTACA 539  
DB 241 TGCTTGTGGCCCTTGGGGGTCAGTACCAAGAGACCCATCCCAAGACCTGCTTACA 300  
QY 540 GAGGCTGCACTTGGAGTGGCTGGAATAATCTGGAGTCCCTGGACCGAGGGGAGGCCCC 599  
DB 301 GAGGCTGCACTTGGAGTGGCTGGAATAATCTGGAGTCCCTGGACCGAGGGGAGGCCCC 360  
QY 600 TGTGAGGACTTTTACAGTTCTCTGTGGGGCTGATTGGAGGAAACCCCTGCGCGAT 659  
DB 361 TGTGAGGACTTTTACAGTTCTCTGTGGGGCTGATTGGAGGAAACCCCTGCGCGAT 420  
QY 660 GGGGCTTCTGCTGGAACACTTCAAGGCTCTGGGACCAAAACCGAGCATCTAGAG 719  
DB 421 GGGGCTTCTGCTGGAACACTTCAAGGCTCTGGGACCAAAACCGAGCATCTAGAG 480

QY 720 CACCTGCTGAAAACACACCTTCACTCCAGAGTGAAGTGAAGAGACAGAGCCG 779  
DB 481 CACTGCTTGAAAACACACCTTCACTCCAGAGTGAAGTGAAGAGACAGAGCCG 540  
QY 780 TTCTACCTATCTTGGCTTACAGGTTGAGAGCCATTTAGAGCTGGAGCCCACTGAGA 839  
DB 541 TTCTACCTATCTTGGCTTACAGGTTGAGAGCCATTTAGAGCTGGAGCCCACTGAGA 600  
QY 840 GACCTCATGAGAAAGTTGGTGTGGAACATTAGGGGGCCCTGGAGCCAGGACAACTTT 899  
DB 601 GACCTCATGAGAAAGTTGGTGTGGAACATTAGGGGGCCCTGGAGCCAGGACAACTTT 660  
QY 900 ATGAGAGTTGTAAGCACTAGACAGGACCTTACAGGGCCACCCCAATCTTCACTGAC 959  
DB 661 ATGAGAGTTGTAAGCACTAGACAGGACCTTACAGGGCCACCCCAATCTTCACTGAC 720  
QY 960 ATCAGTCCGACTTAAAGATTCCAAACAGCAATGTTATCAGGTGAGCCAGTCTGGGCTC 1019  
DB 721 ATCAGTCCGACTTAAAGATTCCAAACAGCAATGTTATCAGGTGAGCCAGTCTGGGCTC 780  
QY 1020 TTTTGGCCCTCCGGATTAATTAACAAGAACTGGCAATGAGAAAGTGCACCTGCC 1079  
DB 781 TTTTGGCCCTCCGGATTAATTAACAAGAACTGGCAATGAGAAAGTGCACCTGCC 840  
QY 1080 TATCTGATTTACATGAGAGAACTGGGATGCTGTGGGGCGGCCCACTTCAAGAG 1139  
DB 841 TATCTGATTTACATGAGAGAACTGGGATGCTGTGGGGCGGCCCACTTCAAGAG 900  
QY 1140 GAGCAGATGACAGAGTGTGAGATTGAGATACAGTGGCCCACTCAAGTCCCGAG 1199  
DB 901 GAGCAGATGACAGAGTGTGAGATTGAGATACAGTGGCCCACTCAAGTCCCGAG 960  
QY 1200 GACCAAGCGCGGAGAGAGAGAAATCTACCAAGATGAGATTTCGAGCTGACAGCT 1259  
DB 961 GACCAAGCGCGGAGAGAGAGAAATCTACCAAGATGAGATTTCGAGCTGACAGCT 1020  
QY 1260 CTGGCCCTCTCATGAGACTGGCTTGAATCTGTCTTTTCTGCTGACCATTTGAGTTG 1319  
DB 1021 CTGGCCCTCTCATGAGACTGGCTTGAATCTGTCTTTTCTGCTGACCATTTGAGTTG 1080  
QY 1320 AGTGACTTGAAGCTGTGGTGTGATGAGATGAGATTATTTGACAGAGTGTCAAGCTC 1379  
DB 1081 AGTGACTTGAAGCTGTGGTGTGATGAGATGAGATTATTTGACAGAGTGTCAAGCTC 1140  
QY 1380 ATCAACCGACCGGACCAAGCAATCTGAACAATTTACTGATCTGAGACCTGGGCAAAAG 1439  
DB 1141 ATCAACCGACCGGACCAAGCAATCTGAACAATTTACTGATCTGAGACCTGGGCAAAAG 1200  
QY 1440 ACNACTCAAGCTTGAAGCCGACTTTGAGTGTGACAAAGAGAGCTGTGAGACCTTC 1499  
DB 1201 ACNACTCAAGCTTGAAGCCGACTTTGAGTGTGACAAAGAGAGCTGTGAGACCTTC 1260  
QY 1500 TATGCACTTAAGAGTCTGTGTGCGGAGGTGACAGCTGTCACTCCAAACAGATGAC 1559  
DB 1261 TATGCACTTAAGAGTCTGTGTGCGGAGGTGACAGCTGTCACTCCAAACAGATGAC 1320  
QY 1560 GCCCTTGACTTGGCTTTGGGGTCCCTCTTGTGAAAGCCACGTTTGAACCGGCAAAAGCAA 1619  
DB 1321 GCCCTTGACTTGGCTTTGGGGTCCCTCTTGTGAAAGCCACGTTTGAACCGGCAAAAGCAA 1380  
QY 1620 GAATATGACAGAGGATGATCAGCGAAATCCGACCGCAATTTGAGAGGCGCTGGAGAG 1679  
DB 1381 GAATATGACAGAGGATGATCAGCGAAATCCGACCGCAATTTGAGAGGCGCTGGAGAG 1440  
QY 1680 CTGGTTGATGATGAGAGAGAGCCGCGACGAGCCAGAGAGAGAGAGAGATGCACTTAT 1739  
DB 1441 CTGGTTGATGATGAGAGAGAGCCGCGACGAGCCAGAGAGAGAGAGATGCACTTAT 1500  
QY 1740 GATATGATGATTTCCAGACTTATCTGAGAGCCCAAGAGCTGATGATGTTATGAC 1799  
DB 1501 GATATGATGATTTCCAGACTTATCTGAGAGCCCAAGAGCTGATGATGTTATGAC 1560  
QY 1800 GGGTACGAATTTCTGAGATTTCTTTCATAAATGATGATTTGTACAACTTCTCT 1859



Db 1561 GGGAGCAAAATTTCTGAGATTTCTTTCTTCCAAAACATGTTGAAATTTTGACACTTCTCT 1620  
Qy 1860 GCCAAGTTATGCTGACCAAGCTCCGAGAGCTTCCAGCCGAGACCAAGTGAGATAC 1919  
Db 1621 GCCAAGTTATGCTGACCAAGCTCCGAGAGCTTCCAGCCGAGACCAAGTGAGATAC 1680  
Qy 1920 CCCAGACATGATGCTCTACTACTCTTCAACTAAGAAATGATGCTTCCCGCTGGC 1979  
Db 1681 CCCAGACATGATGCTCTACTACTCTTCAACTAAGAAATGATGCTTCCCGCTGGC 1740  
Qy 1980 ATCTGAGAGCCCTCTTCTATGCCCCGAGACCCCAAGCCCTTGAATCTTGAGTGCATC 2039  
Db 1741 ATCTGAGAGCCCTCTTCTATGCCCCGAGACCCCAAGCCCTTGAATCTTGAGTGCATC 1800  
Qy 2040 GGTGTGCTCATGAGCCATGAGTTGACGATGCTTTGATGACCAAGGCGCGAGTATGAC 2099  
Db 1801 GGTGTGCTCATGAGCCATGAGTTGACGATGCTTTGATGACCAAGGCGCGAGTATGAC 1860  
Qy 2100 AAAGAAAGGAAACCTGCGGCTGCTGAGCAATGAGTCCCTGAGAGCTTCCGGAACAC 2159  
Db 1861 AAAGAAAGGAAACCTGCGGCTGCTGAGCAATGAGTCCCTGAGAGCTTCCGGAACAC 1920  
Qy 2160 ACCGCTGCATGAGAGAAAGATCAATCAATCAAGGTCAATGAGGAGAGGCTCAAGCC 2219  
Db 1921 ACCGCTGCATGAGAGAAAGATCAATCAATCAAGGTCAATGAGGAGAGGCTCAAGCC 1980  
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Db 2581 TTCCCATAGGAAAGAGTCTGCC 2602

RESULT 7

US-09-978-189-525  
; Sequence 525, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gueney, Austin J.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      72.9%; Score 2461.2; DB 10; Length 2602;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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QY      420 ACCGAGCTGAGGTGATCTTAGAGAGTGCCTCTTACTGCTGAGCTTGCCTTCTTGGGC 479
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DB      181 ACGCAGCTGAGGTGATCTTAGAGAGTGCCTCTTACTGCTGAGCTTGCCTTCTTGGGC 240
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QY      540 GAGGCTGATTCGAGTGGCTGAGAAATCTGGAATCCCTGGAACGAGGGGTGAGCCCC 599
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Db 421 GGGGGTCTGCTGGAACACCTTCAACAGCTCTGGGACCAAAACCGAGCCATCTGAG 480  
Qy 720 CACCTGCTTAAAAACACCACTTCAACAGCTGAGTGAAGTGAAGAGAGAGAGAGAGAGAG 779  
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Qy 1080 TATCTGATTTACATGAGAACTGGGAGTCTGTGGTGGGGGCGCCCACTCCAGAG 1139  
Db 841 TATCTGATTTACATGAGAACTGGGAGTCTGTGGTGGGGGCGCCCACTCCAGAG 900  
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Db 2041 TACCAAGCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100  
Qy 2340 AACCAACAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2399  
Db 2101 AACCAACAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2160  
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DB 2521 ATTCACTGACATCTTTCCGTGACCCCTGAGAGAGGTCTGGTGGGGAGGCCAG 2580  
QY 2820 TTCCCATAGGAGAGGTCTGCC 2841  
DB 2581 TTCCCATAGGAGAGGTCTGCC 2602

## RESULT 8

US-09-978-608A-525

Sequence 525, Application US/09978608A

Publication No. US20030045462A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarolf, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C22  
CURRENT APPLICATION NUMBER: US/09/978.608A  
PRIORITY FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 525  
LENGTH: 2602  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-525

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
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DB 961 GACCAAGGCGGCGACAGAGAGAGATCTACCAAGATGAGATTTGAGAGCTGAGGCT 1020  
QY 1260 CTGGCGCCCTCCATGAGCTGGCTTGAAGTCTGTCTTCTGTGCTGACCAATTGAGGTTG 1319  
DB 1021 CTGGCGCCCTCCATGAGCTGGCTTGAAGTCTGTCTTCTGTGCTGACCAATTGAGGTTG 1080  
QY 1320 AGTGACTTGAAGCTGTGGTGGTGTATGAGAGATGATTTTGGAGAGAGGTTCAGAGCTC 1379  
DB 1081 AGTGACTTGAAGCTGTGGTGGTGTATGAGAGATGATTTTGGAGAGAGGTTCAGAGCTC 1140  
QY 1380 ATCAACCGACCGAGAACCAAGCATCTGAAACAATTACCTGATCTGAAACCTGTGCAAAAG 1439  
DB 1141 ATCAACCGACCGAGAACCAAGCATCTGAAACAATTACCTGATCTGAAACCTGTGCAAAAG 1200  
QY 1440 ACAACCTCAAGCTTGAAGCGAGCTTGAAGTCTGCAAGAGAGAGCTGTGAGAGCCCTC 1499  
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QY 1500 TATGAGACTAAGAGTCTGTGTCGAGAGTGGACAGCTGCACTTCCAAACGAGTGAAC 1559  
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1680 CTGGTTGGATGGAAGAGACCCGCGCAGGCGCAAGGAGAGAGATGCACTTAT 1739  
1441 CTGGTTGGATGGAAGAGACCCGCGCAGGCGCAAGGAGAGAGATGCACTTAT 1500  
1740 GATATGATGTTTCCAGACTTATCTGAGACCCCAAGAGCTGATGATGTTATGAC 1799  
1501 GATATGATGTTTCCAGACTTATCTGAGACCCCAAGAGCTGATGATGTTATGAC 1560  
1800 GGGTACGAATTTCTGAAGATTTCTTCTGAAAACATGTTGATTTGATCACTTCT 1859  
1561 GGGTACGAATTTCTGAAGATTTCTTCTGAAAACATGTTGATTTGATCACTTCT 1620  
1860 GCCAAGTTATGCTGACCAAGCTCCGCAAGCTCCGCAAGCTCCGCAAGCTGAC 1919  
1621 GCCAAGTTATGCTGACCAAGCTCCGCAAGCTCCGCAAGCTGACCAAGCTGAC 1680  
1920 CCCGACAGTGAATGCTGACCTTCACTTCACTGATGATGATGATGATGATGAT 1979  
1681 CCCGACAGTGAATGCTGACCTTCACTTCACTGATGATGATGATGATGATGAT 1740  
1980 ATCTGCAAGGCCCCCTTCTATGCTGCGCAACCAACCCCAAGGCTTGAACCT 2039  
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2040 GGTGCTGATGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099  
1801 GGTGCTGATGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
2100 AAAAGAGGAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2159  
1861 AAAAGAGGAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
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2220 CGCGAGAGCTGCGGAGGAGAACTGCTGCAAGGAGGAGGAGGAGGAGGAGGAG 2279  
1981 CGCGAGAGCTGCGGAGGAGAACTGCTGCAAGGAGGAGGAGGAGGAGGAGGAG 2040  
2280 TACAAAGATGCTGAGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2339  
2041 TACAAAGATGCTGAGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100  
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2400 AGCTCTCAAGAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2459  
2161 AGCTCTCAAGAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220  
2460 AGCTCTCAAGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2519  
2221 AGCTCTCAAGCTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280  
2520 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2579  
2281 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2340  
2580 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2639  
2341 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2400  
2640 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2699  
2401 AACCAAGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2460  
2700 TCAATCAACAATTTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2759  
2461 TCAATCAACAATTTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2520

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Db 2521 ATTCAGTGAATCTTTCCGCTGACCTGCTGAGAAAGGCTGGGTGGGAGGCCAG 2580  
Query 2820 TTCCATAGGAAGAGCTGACC 2841  
Db 2581 TTCCATAGGAAGAGCTGACC 2602

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US-09-978-585A-525  
; Sequence 525, Application US/09978585A  
; Publication No. US2003004963A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gueney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kjaavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Thomas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 525  
; LENGTH: 2602  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-978-585A-525

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Query 360 CTCTGCTAGAGACTATGATGAGGATTTCCAGAGGAGCAAGACAGCTGTTAGGCTGACGC 419  
Db 121 CTGGAGCTGGAGCAAGCAAGTGGGATTTCCAGAGGAGCAAGACAGCTGTTAGGCTGACGC 180  
Query 420 AGCAGAGCTGAGCTGCTTACAGAGGCTCTTCTATCTGCTGCTGCTGCTGCTGCTG 479  
Db 181 AGCAGAGCTGAGCTGCTTACAGAGGCTCTTCTATCTGCTGCTGCTGCTGCTGCTGCTG 240  
Query 480 TGCCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 539  
Db 241 TGCCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 300  
Query 540 GAGGCTGATTCAGAGTGGCTGAGAAATCTGAGAGTCCCTGAGACCGAGGAGTGAAGCCC 599  
Db 301 GAGGCTGATTCAGAGTGGCTGAGAAATCTGAGAGTCCCTGAGACCGAGGAGTGAAGCCC 360

QY 600 TGTGAGACCTTTACCAAGTTCTCTGTGGGGGCTGGAATTCGAGGAACCCCTGCCCCGAT 659  
DB 361 TGTGAGACCTTTACCAAGTTCTCTGTGGGGGCTGGAATTCGAGGAACCCCTGCCCCGAT 420  
QY 660 GGGCGTTCTCGTGAACAACCTTCAACAGCCTCTGGAGCCAAACAGGCGCATCTGAAG 719  
DB 421 GGGCGTTCTCGTGAACAACCTTCAACAGCCTCTGGAGCCAAACAGGCGCATCTGAAG 480  
QY 720 CACCTGCTTGAACCAACCTTCAACAGCCTCTGGAGCCAAACAGGCGCATCTGAAG 779  
DB 481 CACCTGCTTGAACCAACCTTCAACAGCCTCTGGAGCCAAACAGGCGCATCTGAAG 540  
QY 780 TTCTACTATCTTCCCTACAGGTGAGAGCGCATTTGAGAGCTGGAGCCGACGACCTGAG 839  
DB 541 TTCTACTATCTTCCCTACAGGTGAGAGCGCATTTGAGAGCTGGAGCCGACGACCTGAG 600  
QY 840 GACCTCATTTGAGAGATTTGGTGGTTGGAACATTACGGGGCCCTGGAGCCAGAACATT 899  
DB 601 GACCTCATTTGAGAGATTTGGTGGTTGGAACATTACGGGGCCCTGGAGCCAGAACATT 660  
QY 900 ATGAGAGTGTGAAGGAGTGAAGGAGCCTTACAGGGCCACCCCATTTCTTCACTGCTAC 959  
DB 661 ATGAGAGTGTGAAGGAGTGAAGGAGCCTTACAGGGCCACCCCATTTCTTCACTGCTAC 720  
QY 960 ATGAGAGTGTGAAGGAGTGAAGGAGCCTTACAGGGCCACCCCATTTCTTCACTGCTAC 1019  
DB 721 ATGAGAGTGTGAAGGAGTGAAGGAGCCTTACAGGGCCACCCCATTTCTTCACTGCTAC 780  
QY 1020 TTTCTGCCCCCTCTGGAGTTACTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
DB 781 TTTCTGCCCCCTCTGGAGTTACTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 840  
QY 1080 TATCTGAGTATCAATGAGAACTGGGGATCTGCTGGGTGGGGCCCACTTCAAGAGG 1139  
DB 841 TATCTGAGTATCAATGAGAACTGGGGATCTGCTGGGTGGGGCCCACTTCAAGAGG 900  
QY 1140 GACAGAGTGCAGAGGCTGAGGTTGAGATACAGCTGGCCAAACATCAAGTGGCCAG 1199  
DB 901 GACAGAGTGCAGAGGCTGAGGTTGAGATACAGCTGGCCAAACATCAAGTGGCCAG 960  
QY 1200 GACAGAGGCGCAGCAGAGAGAAATCTACACAAAGTGAAGATTTGAGAGTGGAGCT 1259  
DB 961 GACAGAGGCGCAGCAGAGAGAAATCTACACAAAGTGAAGATTTGAGAGTGGAGCT 1020  
QY 1260 CTGGCGCCCTCCATGAGCTGGCTTGAATCTGCTTTCTTCTGCTGCAATTTGAGAGT 1319  
DB 1021 CTGGCGCCCTCCATGAGCTGGCTTGAATCTGCTTTCTTCTGCTGCAATTTGAGAGT 1080  
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QY 1620 GAAATTCAGAGGGGATGATCAGGAAATCCGAGCCGATTTGAGAGGCGCTGGAGCAG 1679  
DB 1381 GAAATTCAGAGGGGATGATCAGGAAATCCGAGCCGATTTGAGAGGCGCTGGAGCAG 1440

QY 1680 CTGATTTGATGATGAGAGAGACCCGACGAGCCAAAGAGAAAGACAGATCCATCTAT 1739  
DB 1441 CTGATTTGATGATGAGAGAGACCCGACGAGCCAAAGAGAAAGACAGATCCATCTAT 1500  
QY 1740 GATATGATTTGTTTCCAGACTTTTATCTGAGGCCAAAGAGCTGATGATTTATGAC 1799  
DB 1501 GATATGATTTGTTTCCAGACTTTTATCTGAGGCCAAAGAGCTGATGATTTATGAC 1560  
QY 1800 GGGTACGAAATTTTGAAGATTTCTTCCAAACATGTTGAATTTGACAACTTCTCT 1859  
DB 1561 GGGTACGAAATTTTGAAGATTTCTTCCAAACATGTTGAATTTGACAACTTCTCT 1620  
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DB 1621 GCCAAGTATGATGATGAGCAGCTCCGACAGCTCCAGCCGAGACAGTGAAGTAC 1680  
QY 1920 CCCAGACAGTGAATGCTTACTACTTCCAACTTAAGATGATGCTTTCCCGCTGGC 1979  
DB 1681 CCCAGACAGTGAATGCTTACTACTTCCAACTTAAGATGATGCTTTCCCGCTGGC 1740  
QY 1980 ATCTGCAAGGCCCCCTTCTATGCCCCGCAACACCCCAAGGCCCTGAACCTTGGTGGCATC 2039  
DB 1741 ATCTGCAAGGCCCCCTTCTATGCCCCGCAACACCCCAAGGCCCTTGAACCTTGGTGGCATC 1800  
QY 2040 GGTGTGATGATGAGGATGATGAGCAGATGCTTGAAGCAGAGGCGCAGATGAC 2099  
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QY 2100 AAGAGAGGAACTCTGCGGCCCTGTGTGAGAAATGAGTCCCTGAGCCTTCCGAAACAC 2159  
DB 1861 AAGAGAGGAACTCTGCGGCCCTGTGTGAGAAATGAGTCCCTGAGCCTTCCGAAACAC 1920  
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DB 1981 CGCAGACGCTGGGGAGAACATTTGCTGACAAAGGGGGCTGAAGGCTGCTCAATGCT 2040  
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DB 2041 TACAAAGCATGCTGAGAAAGCATGAGGGAGAGACCACTGCAAGCCTGGGGCTCAAC 2100  
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DB 2101 AACCAACAGCTCTTCTGAGGAAATTTGCCAGGTGAGTGGCTGGCTCCGACACAGAG 2160  
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DB 2281 AACCCAGGAGAGTGTGAGGAGTGTGAGCCTGGAATGAGGAGAAATGCGCAGCTGT 2340  
QY 2580 CACAGACCTGGGGAGCTCTCTGCAAAAGCTTTGCTTTGGTGGAGAGAGCA 2639  
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QY 2640 ATGCAAGCTGGGCTGTGATGCTTCCCGCCAGAGGTGACATGATGACAGCCTTCC 2699  
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QY 2700 TCAATCAACAAATGAGCTCTGCTTTGGGGGGGAGCCCTGCTCCAGAGAGGCCCAAC 2759  
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QY 2760 ATTCACTGTGACATCTTCTCGTGTCAACCTGCTGAGAGAGGCTGTGGTGGAGGCGCAG 2819



Db 2521 ATTCACTGTGACATCTTTCGTGTCACTCCCTGGAGAGGCTGTGGTGGGAGGCGCAG 2580  
QY 2820 TTCCCATAGGAGAGAGCTCTGCC 2841  
Db 2581 TTCCCATAGGAGAGAGCTCTGCC 2602

## RESULT 10

US-09-978-191A-525  
Sequence 525, Application US/09978191A  
Publication No. US2003050239A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978,191A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2465; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 121 CTGGAGCTGGAGCAAGCTGGGATTCAGAAAGGAGCAAGACAGCTGTTAGGCTCAGCG 180

QY 420 ACGCAGCTGAGAGTGTCTTAGCAGGTGCTCTACTGTGGCTGCACTGCTTGAGC 479  
DB 181 ACGCAGCTGAGAGTGTCTTAGCAGGTGCTCTACTGTGGCTGCACTGCTTGAGC 240  
QY 480 TGCCTTGTGGCCCTTAGGGGTCCAGTACAGAGAGCCATCCCAAGCAGCTTGCCTTACA 539  
DB 241 TGCCTTGTGGCCCTTAGGGGTCCAGTACAGAGAGCCATCCCAAGCAGCTTGCCTTACA 300  
QY 540 GAGGCTGCAATTCAGAGTGTGAGAAAAATCCCTGAGTCCCTGAGCCAGAGGGTGAAGCCCC 599  
DB 301 GAGGCTGCAATTCAGAGTGTGAGAAAAATCCCTGAGTCCCTGAGCCAGAGGGTGAAGCCCC 360  
QY 600 TGTGAGAGCTTTTACCAAGTTCTCTGTGGGGCTGGAATTGAGAGAACCCCTGCGCAT 659  
DB 361 TGTGAGAGCTTTTACCAAGTTCTCTGTGGGGCTGGAATTGAGAGAACCCCTGCGCAT 420  
QY 660 GGGCGTTCTCGCTGGAACACCTTCAACAGCTCTGAGAACAAACAGGCTTACTGAAG 719  
DB 421 GGGCGTTCTCGCTGGAACACCTTCAACAGCTCTGAGAACAAACAGGCTTACTGAAG 480  
QY 720 CACCTGCTTGAAGAACCACTTCAACCTCAGAGAGTGAAGCTGAGAGAGACAGAGCGC 779  
DB 481 CACCTGCTTGAAGAACCACTTCAACCTCAGAGAGTGAAGCTGAGAGAGACAGAGCGC 540  
QY 780 TTCTACCTATCTTGCCTTACAGGTGAGCGCATTTGAGAGAGCTGGAGCCAGCACTGAGA 839  
DB 541 TTCTACCTATCTTGCCTTACAGGTGAGCGCATTTGAGAGAGCTGGAGCCAGCACTGAGA 600  
QY 840 GACCTCATTTAGAGAGATTTGTGTGGAACATTAACGGGCTCTGGAGCAAGACAACTTT 899  
DB 601 GACCTCATTTAGAGAGATTTGTGTGGAACATTAACGGGCTCTGGAGCAAGACAACTTT 660  
QY 900 ATGAGAGTGTGAAGCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959  
DB 661 ATGAGAGTGTGAAGCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 960 ATCAGTCCGCACTTAAGAGTTCCAAACAGCAATGTTATCAGGTGAGAGAGTCTGGGCTC 1019  
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QY 1020 TTTCTGCCCCCTCGGGATTAATACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
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QY 1080 TATCTGAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139  
DB 841 TATCTGAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
QY 1140 GAGCAGATGACAGAGAGTGTGAGAGTGAAGATTAACAGTGGCCAACTACAGTGGCCAG 1199  
DB 901 GAGCAGATGACAGAGAGTGTGAGAGTGAAGATTAACAGTGGCCAACTACAGTGGCCAG 960  
QY 1200 GACCAAGCGCGCGAGAGAGAGAGAGATCTAACCAAGATGAGCAATTCGAGCTGCAAGCT 1259  
DB 961 GACCAAGCGCGCGAGAGAGAGAGAGATCTAACCAAGATGAGCAATTCGAGCTGCAAGCT 1020  
QY 1260 CTGGCGCCCTCCATGAGACTGTGAGTTCCTGCTCTTCTGCTGCAATTTGAGAGTG 1319  
DB 1021 CTGGCGCCCTCCATGAGACTGTGAGTTCCTGCTCTTCTGCTGCAATTTGAGAGTG 1080  
QY 1320 AGTGACTTGAAGCTGTGAGTGTATGAGAGATTAATTTGAGAGAGTGTGAGAGCTC 1379  
DB 1081 AGTGACTTGAAGCTGTGAGTGTATGAGAGATTAATTTGAGAGAGTGTGAGAGCTC 1140  
QY 1380 ATCAACCGACGAGAACCAAGCATCTGAACATTTACCTGATCTGAACCTGTGCAAAAG 1439  
DB 1141 ATCAACCGACGAGAACCAAGCATCTGAACATTTACCTGATCTGAACCTGTGCAAAAG 1200  
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DB 1201 ACAACCTCAAGCTGAGAGAGAGAGCTTTGAGTCTGCAACAAGAGAGCTGAGAGAGCTC 1260  
QY 1500 TATGAGCACTTAAGAGTCTGTGTGCGAGAGTGGCAGAGCTGATCTCAACAGAGATGAC 1559



[illegible]









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Db	961	GACCACGGCGCGAGAGAGAAAGATCTAACACAAGATGAGACATTTGCGACCTGACGCT	1020
QY	1260	CTGGCGCCCTCCATGGAAGCTGGCTTGAAGTTCCTGTCTTCTTGCTGTCAACAATTGGAGTTG	1319
Db	1021	CTGGCGCCCTCCATGGAAGCTGGCTTGAAGTTCCTGTCTTCTTGCTGTCAACAATTGGAGTTG	1080
QY	1320	AGTGACTCTGAGCCCTGTGTGTGTGTATATGGATATGATTTATTTGGACAGGTGTCAAGCTC	1379
Db	1081	AGTGACTCTGAGCCCTGTGTGTGTGTATATGGATATGATTTATTTGGACAGGTGTCAAGCTC	1140
QY	1380	ATCAACCCGACCGAACAAGACCTCTGAACCAATTACCTGATCTGGAACTGTGCAAAAG	1439
Db	1141	ATCAACCCGACCGAACAAGACCTCTGAACCAATTACCTGATCTGGAACTGTGCAAAAG	1200
QY	1440	ACAACCTCAAGCTCTGGACCGACGCTTTGATGTCTGCAACAAGAGCTGTGGAACCTC	1499
Db	1201	ACAACCTCAAGCTCTGGACCGACGCTTTGATGTCTGCAACAAGAGCTGTGGAACCTC	1260
QY	1500	TATGGCACTAAGAAGCTCGTGTGTGCGAAGTGGCGAGACCTGCATCTCCAAACGGATGAC	1559
Db	1261	TATGGCACTAAGAAGCTCGTGTGTGCGAAGTGGCGAGACCTGCATCTCCAAACGGATGAC	1320
QY	1560	GCCCTTGGCTTGTCTTTGGGGTCCCTCTCTTGTAAGGCCACGTTTGAACCGGCAAGCAAA	1619
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QY	1620	GAAATTGCAAGAGGGGATATATCAGCCAAATCCGGACCCGATTTGAGAGAGCCCTGGACAG	1679
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QY	1680	CTGTGTTGGATGATGAGAGAGACCCGCGACGACGCAAGAGAAAGCATGTCCATCTAT	1739
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QY	1740	GATATGATTTGGTTTCCCAAGCTTTATCTGAGCCCAAGAGCTGATGATGTTTATGAC	1799
Db	1501	GATATGATTTGGTTTCCCAAGCTTTATCTGAGCCCAAGAGCTGATGATGTTTATGAC	1560
QY	1800	GGGTACGAAATTTCTGAAGATTCTTCTTCCAAAACATGTGAATTTGTACAACCTCTCT	1859
Db	1561	GGGTACGAAATTTCTGAAGATTCTTCTTCCAAAACATGTGAATTTGTACAACCTCTCT	1620
QY	1860	GCCAAAGTTATGCTGTACCAAGCTCCGCAAGCCTCCAGCTGAGACCAATGAGATGAC	1919
Db	1621	GCCAAAGTTATGCTGTACCAAGCTCCGCAAGCCTCCAGCTGAGACCAATGAGATGAC	1680
QY	1920	CCCCAGACAGTGAAGCCCTACTACTCTTCCAACTAAGATATGATATCTTCCCGCTGGC	1979
Db	1681	CCCCAGACAGTGAAGCCCTACTACTCTTCCAACTAAGATATGATATCTTCCCGCTGGC	1740
QY	1980	ATCTTGACAGGCCCTCTTATGTCGCCGACAACCCCAAGGCCCTGAACTTTCGTGTGATC	2039
Db	1741	ATCTTGACAGGCCCTCTTATGTCGCCGACAACCCCAAGGCCCTGAACTTTCGTGTGATC	1800
QY	2040	GGTGTGTCTATGCGCCATGATGATTTGACGATGCTTTGATATACCAAGGCGCGAGTATGAC	2099
Db	1801	GGTGTGTCTATGCGCCATGATGATTTGACGATGCTTTGATATACCAAGGCGCGAGTATGAC	1860
QY	2100	AAAGAAAGGGAACCTTGCAGGCCCTGTGTGGAGATGATGCTTCCGGGACCTTCCGGAAACAC	2159
Db	1861	AAAGAAAGGGAACCTTGCAGGCCCTGTGTGGAGATGATGCTTCCGGGACCTTCCGGAAACAC	1920
QY	2160	ACGCGCTGATGAGAGAAACAGTACATCAATACCAAGTCAATGGGAGAGGCTCAACGCG	2219
Db	1921	ACGCGCTGATGAGAGAAACAGTACATCAATACCAAGTCAATGGGAGAGGCTCAACGCG	1980
QY	2220	CGCCAGACGCTGGGGGAGAACATTTGCTGACCAACGGGGGGCTGAGAGCTGCTTACAATGCT	2279
Db	1981	CGCCAGACGCTGGGGGAGAACATTTGCTGACCAACGGGGGGCTGAGAGCTGCTTACAATGCT	2040

QY	2280	TACAAAGCATGGCTGAGAAAGCATGGGAGGAGAGCAATCGCAGCCGTGGGGCTCAC	2339
Db	2041	TACAAAGCATGGCTGAGAAAGCATGGGAGGAGAGCAATCGCAGCCGTGGGGCTCAC	21000
QY	2340	AACCAACGACTCTTCTTCGTGGGAATTTGCCAGGTGTGTGCTCTCGATCCGACACAG	2399
Db	2101	AACCAACGACTCTTCTTCGTGGGAATTTGCCAGGTGTGTGCTCTCGATCCGACACAG	2160
QY	2400	AGCTCTCACAGGGGGCTGTGTACCCGACCCCCACAGCCCTGCCCCCTTCCGGTGTCTGGC	2459
Db	2161	AGCTCTCACAGGGGGCTGTGTACCCGACCCCCACAGCCCTGCCCCCTTCCGGTGTCTGGC	2220
QY	2460	ACTCTCTCAACTCCCGGACCTTCCTCGGGGACCTTCGGCTGCTCCGCTCCGCCATG	2519
Db	2221	ACTCTCTCAACTCCCGGACCTTCCTCGGGGACCTTCGGCTGCTCCGCTCCGCCATG	2280
QY	2520	AACCCAGGGACGCTGTGTGTAGGTGTGTAGACTGTATCAGGGAGAAATGCCAGCTGT	2579
Db	2281	AACCCAGGGACGCTGTGTGTAGGTGTGTAGACTGTATCAGGGAGAAATGCCAGCTGT	2340
QY	2580	CACCAAGACTGGGGGACGCTCTCTGTACAAAGCTGTTTGTCTTGGGTTGGGAGAGCA	2639
Db	2341	CACCAAGACTGGGGGACGCTCTCTGTACAAAGCTGTTTGTCTTGGGTTGGGAGAGCA	2400
QY	2640	ATGCAGGTGGGGCTGGGTCTAGTGTCCCTCCCTCCCCACAGGTGACATGATACAGACCTCC	2699
Db	2401	ATGCAGGTGGGGCTGGGTCTAGTGTCCCTCCCTCCCCACAGGTGACATGATACAGACCTCC	2460
QY	2700	TCAATTCACCAATTTGTGCTCTGTGCTTTGGGGGATGCCCTGTGCTCAGACAGCCCCAC	2759
Db	2461	TCAATTCACCAATTTGTGCTCTGTGCTTTGGGGGATGCCCTGTGCTCAGACAGCCCCAC	2520
QY	2760	ATTGACGTGTGCAATCTTTCCGCTGTACCCCTGTCTGTGAAGAGTGTGGGTGGGAGGCCAG	2819
Db	2521	ATTGACGTGTGCAATCTTTCCGCTGTACCCCTGTCTGTGAAGAGTGTGGGTGGGAGGCCAG	2580
QY	2820	TTCCCATGTGAAGAGTCTGCC	2841
Db	2581	TTCCCATGTGAAGAGTCTGCC	2602

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RESULT 13
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Sequence 525, Application US/0999833R
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Ausetin L.
APPLICANT: Hillan, Kenneth U.
APPLICANT: Kijavani, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

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;; TITLE OF INVENTION: Acids Encoding the Same  
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;; CURRENT FILING DATE: 2001-10-24  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;

Best Local Similarity 99.5%; Pred. No. 0; Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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1200 GACGAGCTGAGAGAGAGAGATCTACCAAGATGAGAGATTTGAGAGCTGAGAGCT 1259  
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Db 2101 AACCAACAGCTCTTCTTCTGGGATTTGGCCAGGTGTGTCTGCTGCTGCGACACCAAG 2160  
Qy 2400 AGCTCTCAGAGGGGCTGTGACCGAACCCCAAGCCCTGCGGCTTCCGAGTGGGCT 2459  
Db 2161 AGCTCTCAGAGGGGCTGTGACCGAACCCCAAGCCCTGCGGCTTCCGAGTGGGCT 2220  
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Db 2221 ACTCTCTCAACTCCGCTGACTTCTGCGGCACTTGGGCTGCGCTGCTGCGCTCCCATG 2280  
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Db 2521 ATTCACTGAGCACTTCCGCTGATCCCTGCTGAGAGAGTCTGGGTGGGAGGCTGAG 2580  
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Db 2581 TTCCATAGGAGAGAGTCTGCC 2602

RESULT 14  
US-09-981-915A-525  
; Sequence 525, Application US/09981915A  
; Publication No. US20030054986A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flivaeroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Thomas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C12  
; CURRENT APPLICATION NUMBER: US/09/981, 915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 121 CTGGAGCTGGAGCAAGCTGGGATTCAGAAAGGGGCAAGACAGTTGAGGCTTACGC 180  
QY 420 AGCAGCTGGAGCTGGATTCGGAAGGGGCTCTTACGCTGGGCTTACGCTTGGGC 479  
DB 181 AGCAGCTGGAGCTGGATTCGGAAGGGGCTCTTACGCTGGGCTTACGCTTGGGC 240  
QY 480 TGCCTTGTGGGCTTGAAGGCTTCAAGACAGACCCATCCACAGCACTGCTTACA 539  
DB 241 TGCCTTGTGGGCTTGAAGGCTTCAAGACAGACCCATCCACAGCACTGCTTACA 300  
QY 540 GAGGCTGCAATTCAGTGGCTGGAATAATCTTGAAGTCCCTTGAAGCTGAGGGTGAAGCCC 599  
DB 301 GAGGCTGCAATTCAGTGGCTGGAATAATCTTGAAGTCCCTTGAAGCTGAGGGTGAAGCCC 360  
QY 600 TGTGAGGACTTTTACAGATTCCTGTGGGGCTGGAATTGGAAGAAACCCCTGAGCAT 659  
DB 361 TGTGAGGACTTTTACAGATTCCTGTGGGGCTGGAATTGGAAGAAACCCCTGAGCAT 420  
QY 660 GGGCGTTCTGCTGGAACACTTCAACAGCTCTGGGACCAAAACAGGCTTACTGAAG 719  
DB 421 GGGCGTTCTGCTGGAACACTTCAACAGCTCTGGGACCAAAACAGGCTTACTGAAG 480  
QY 720 CACTGCTTGAAGAACCACTTCAACAGCTTCAAGCACTGGAAGCTGAGCAAGACAGGCGC 779  
DB 481 CACTGCTTGAAGAACCACTTCAACAGCTTCAAGCACTGGAAGCTGAGCAAGACAGGCGC 540  
QY 780 TTCTACCTATCTTGGCTTCAAGGAGGAGGCAATTTGAGAGCTGAGGAGCCAGGCACTGAG 839  
DB 541 TTCTACCTATCTTGGCTTCAAGGAGGAGGCAATTTGAGAGCTGAGGAGCCAGGCACTGAG 600  
QY 840 GACCTCATTTGAGAAAGATTTGGTGGTGAACATTTACGGGGCCCTGGGACCAAGACAACTTT 899



Db 601 GACCTATTGAGAAAGTTGGTGGTGGAACTTACCGGGGCCCTGGAGCAGAGCAACTTT 660  
Qy 900 ATGAGAGTGTGAGGCAAGTACGAGGAGCCTTACAGGGCCACCCCATTTCTTACCGTCTAC 959  
Db 661 ATGAGAGTGTGAGGCAAGTACGAGGAGCCTTACAGGGCCACCCCATTTCTTACCGTCTAC 720  
Qy 960 ATCAGTCCGAGCTTAAAGATTCCACAGCAATGTTATCCAGGTGACCAAGTCTGGGCTC 1019  
Db 721 ATCAGTCCGAGCTTAAAGATTCCACAGCAATGTTATCCAGGTGACCAAGTCTGGGCTC 780  
Qy 1020 TTTCTGCGCTCTGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
Db 781 TTTCTGCGCTCTGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTCTCACTGCC 840  
Qy 1080 TATCTGATTAATCAATGAGAACTGGGAGATGCTGCGGTGGGCGGCCCACTTCAGAGG 1139  
Db 841 TATCTGATTAATCAATGAGAACTGGGAGATGCTGCGGTGGGCGGCCCACTTCAGAGG 900  
Qy 1140 GAGCAGATGAGAGAGTGTCTGAGATTGAGATACAGTCTGGCCAACTACAGTGGCCAG 1199  
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Qy 1200 GACCAAGCGGCGCAGAGAGAGATCTTACCAAGATGAGCAATTCGAGCTGCAAGCT 1259  
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Qy 1260 CTGGCGCCCTCCATGAGACTGGCTTGAAGTCTGTCTTCTTCTGTCTCAACATTTGAGATTG 1319  
Db 1021 CTGGCGCCCTCCATGAGACTGGCTTGAAGTCTGTCTTCTTCTGTCTCAACATTTGAGATTG 1080  
Qy 1320 AGTGAATCTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1379  
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Qy 1380 ATCAACCGCAGCAGAGCAAGCATCTGAGCAATTAACCTGATCTGAGCACTGGTCAAAAG 1439  
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Qy 1560 GGCCTTGGCTTGTGGGGTCCCTCTTGTGTAAGGCCACGTTTGAACGGGCAAGCAAA 1619  
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Qy 2040 GGTGTGTATGGGCGCATGATGATGACGATGCTTGTATGATGACCAAGGCGGAGTATGAC 2099  
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Db 1921 ACGGCTGCAATGAGAGAACTTCAATCAATACAGGTCAATGGGAGAGGCTCAACGGC 1980  
Qy 2220 CGCAGACGCTGGGAGGAACTTGTCTGCAACGGGAGGCTGAAAGGCTGCTCAATGCT 2279  
Db 1981 CGCAGACGCTGGGAGGAACTTGTCTGCAACGGGAGGCTGAAAGGCTGCTCAATGCT 2040  
Qy 2280 TACAAAGCATGCTGAGAAAGCATGAGGAGAGCAGCAACTGCAAGCCGTGGGCTCAC 2339  
Db 2041 TACAAAGCATGCTGAGAAAGCATGAGGAGAGCAGCAACTGCAAGCCGTGGGCTCAC 2100  
Qy 2340 AACCAACAGCTCTTCTTGTGGGATTTGCGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2399  
Db 2101 AACCAACAGCTCTTCTTGTGGGATTTGCGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2160  
Qy 2400 AGCTCTCAGAGGAGGCTGTGTGACCCGACCCCAAGCCCTGCGGCTTCCGCGTGTGGG 2459  
Db 2161 AGCTCTCAGAGGAGGCTGTGTGACCCGACCCCAAGCCCTGCGGCTTCCGCGTGTGGG 2220  
Qy 2460 ACTCTCTCAACTCCCGTGAATCTTCTGCGGCACTTGTGGCTGTGCGCTTCCCGATG 2519  
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Db 2281 AACCCAGGCGAGCTGTGTGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340  
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RESULT 15  
US-09-978-824-525  
; Sequence 525, Application US/09978824  
; Publication No. US20030055216A1  
GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C14  
CURRENT APPLICATION NUMBER: US/09/978,824  
PRIOR FILING DATE: 2001-10-17  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 72.9%; Score 2461.2; DB 10; Length 2602;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2469; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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420 AGGACACTGAGAGCTGCTTAGAGGCTCTCTAGCTGCTGCTCAAGCTGTAGGCTCAAGC 419  
181 AGGACACTGAGAGCTGCTTAGAGGCTCTCTAGCTGCTGCTCAAGCTGTAGGCTCAAGC 240  
480 TGGCTTGTGGCCCTTAGAGGCTCAGTACACAGAGACCCATCCACAGACCTGCTTAC 539  
241 TGGCTTGTGGCCCTTAGAGGCTCAGTACACAGAGACCCATCCACAGACCTGCTTAC 300  
540 GAGGCTGCTTGTAGTGTGAGTAAATCTTGAAGTCCCTGAGACCGAGGGGTGAGCCCC 599  
301 GAGGCTGCTTGTAGTGTGAGTAAATCTTGAAGTCCCTGAGACCGAGGGGTGAGCCCC 360  
600 TGTGAGAGCTTTACAGAGTCTCTGTGGGGGCTGAGATTGAGGAAACCCCTGCTGAGT 659  
361 TGTGAGAGCTTTACAGAGTCTCTGTGGGGGCTGAGATTGAGGAAACCCCTGCTGAGT 420  
660 GGGGCTTCTGCTGAGAACCTTCAACAGCTCTGGAGCCAAACAGGCTATCTGAG 719

421 GGGGCTTCTGCTGAGAACCTTCAACAGCTCTGGAGCCAAACAGGCTATCTGAG 480  
720 CAGCTGCTTGAAGAACCACTTCAACAGAGTGAAGCTGAGAGAACCAAGCCG 779  
481 CAGCTGCTTGAAGAACCACTTCAACAGAGTGAAGCTGAGAGAACCAAGCCG 540  
780 TTCTACCTATCTTGGCTTACAGGAGGAGGCTTGAAGAGCTGGAGCCAGCCAGTGA 839  
541 TTCTACCTATCTTGGCTTACAGGAGGAGGCTTGAAGAGCTGGAGCCAGCCAGTGA 600  
840 GACCTCATTGAGAGATGAGGCTTGAAGATTTACGGGGCTTGAAGAACCACTT 899  
601 GACCTCATTGAGAGATGAGGCTTGAAGATTTACGGGGCTTGAAGAACCACTT 660  
900 ATGAGAGTGTGAAGCAGTACAGAGGAGCTTACAGGAGCCATTTCTTACCTGCTAC 959  
661 ATGAGAGTGTGAAGCAGTACAGAGGAGCTTACAGGAGCCATTTCTTACCTGCTAC 720  
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1020 TTCTGCTTCTGAGGATTAATTAAGAGAGTCAAGTGAAGAGTCTCACTGCT 1079  
781 TTCTGCTTCTGAGGATTAATTAAGAGAGTCAAGTGAAGAGTCTCACTGCT 840  
1080 TATCTGATTAATTAAGAGAGTCAAGGAGTCTGAGGAGGAGGAGGAGGAGGAGG 1139  
841 TATCTGATTAATTAAGAGAGTCAAGGAGTCTGAGGAGGAGGAGGAGGAGGAGG 900  
1140 GAGCAGATGAGAGGAGTCTGAGGAGTCAAGGAGTCAAGGAGGAGGAGGAGGAGG 1199  
901 GAGCAGATGAGAGGAGTCTGAGGAGTCAAGGAGTCAAGGAGGAGGAGGAGGAGG 960  
1200 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1259  
961 GAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020  
1260 CTGGGCTTCTGAGGAGTCAAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1319  
1021 CTGGGCTTCTGAGGAGTCAAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1080  
1320 AGTGACTTGAAGGAGTCTGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 1379  
1081 AGTGACTTGAAGGAGTCTGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 1140  
1380 ATCAACCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1439  
1141 ATCAACCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
1440 ACACCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499  
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1500 TATGACCTTAAGAGGAGTCTGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGG 1559  
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1560 GGCCTTGTGCTTGTGGGAGTCCCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1619  
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1680 CTGATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1739  
1441 CTGATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500  
1740 GATATGATTTGATTTCCAGACTTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1799  
1501 GATATGATTTGATTTCCAGACTTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560

Search completed: July 3, 2004, 20:05:48  
Job time : 1396 secs

QY	1800	GGGATACGAAATTTGGAAGATTCTTTCTTCCAAAACAGTGAATTGTAACAATTCTCT	1859
Db	1551	GGGATACGAAATTTGGAAGATTCTTTCTTCCAAAACAGTGAATTGTAACAATTCTCT	1620
QY	1860	GCCAAAGTTATGCTGACCACTCCGCAAGCTCTCCAGCCGACACAGTGAACATGACC	1919
Db	1621	GCCAAAGTTATGCTGACCACTCCGCAAGCTCTCCAGCCGACACAGTGAACATGACC	1680
QY	1920	CCCCGACAGTGAAGGCTTACTACCTTCCACTGAAGATGAGATCGTCTTCCCGCTGGC	1979
Db	1661	CCCCGACAGTGAAGGCTTACTACCTTCCACTGAAGATGAGATCGTCTTCCCGCTGGC	1740
QY	1980	ATCTCGACAGGCCCCCTTCTCTATGCCCCGACACACCCCAAGGCGCTGAACCTTCGATGAC	2039
Db	1741	ATCTCGACAGGCCCCCTTCTCTATGCCCCGACACACCCCAAGGCGCTGAACCTTCGATGAC	1800
QY	2040	GGTGTGTCTATGAGGCCATGAGTTGACGCAATGCTTTGATGACCAAGGCGCGATATGAC	2099
Db	1801	GGTGTGTCTATGAGGCCATGAGTTGACGCAATGCTTTGATGACCAAGGCGCGATATGAC	1860
QY	2100	AAAGAAAGGGAACCTCGCGGCCCTGGTGGGAGATGATGCTTCGGGAGCTTCGCGAACAC	2159
Db	1861	AAAGAAAGGGAACCTCGCGGCCCTGGTGGGAGATGATGATGCTTCGGGAGCTTCGCGAACAC	1920
QY	2160	ACGGCTCTGATGAGAGAACATGACATCAATCAATACAGGTCAATGCGGAGAGGCTCAACCGC	2219
Db	1921	ACGGCTCTGATGAGAGAACATGACATCAATCAATACAGGTCAATGCGGAGAGGCTCAACCGC	1980
QY	2220	CGCCGAGAGGCTGGGGGGAGAACATTGCTGACCAAGGGGGGCTGAAGGCGCTCAAAATGCT	2279
Db	1981	CGCCGAGAGGCTGGGGGGAGAACATTACTGACCAAGGGGGGCTGAAGGCGCTCAAAATGCT	2040
QY	2280	TACAAAGCATGCTGAGAAAGCATGGGAGAGAGCAGCACTGCCAGCCGTGCGCTCAACC	2339
Db	2041	TACAAAGCATGCTGAGAAAGCATGGGAGAGAGCAGCACTGCCAGCCGTGCGCTCAACC	2100
QY	2340	AACCAACCAAGCTTTCTTGTGTGGGATTTTGCCCAAGTGTGTGTCTGGTCCGACACCAAG	2399
Db	2101	AACCAACCAAGCTTTCTTGTGTGGGATTTTGCCCAAGTGTGTGTCTGGTCCGACACCAAG	2160
QY	2400	AGCTCTCAGAGGGGCTGGTGAACCAACCCCAACAGCCCTGACCGCTTCGCGTCTGGGC	2459
Db	2161	AGCTCTCAGAGGGGCTGGTGAACCAACCCCAACAGCCCTGACCGCTTCGCGTCTGGGC	2220
QY	2460	ACTCTCTCCAACTCCCGTGACTTCTCTGCGGCACTTTCGCTGCGCTCTGCGTCTCCCAATG	2519
Db	2221	ACTCTCTCCAACTCCCGTGACTTCTCTGCGGCACTTTCGCTGCGCTCTGCGTCTCCCAATG	2280
QY	2520	AACCAAGGCGACCTGTGTGAGGTGTGTGATGACCTGGAATCAAGGGAGAAATGCCAGAGCT	2579
Db	2281	AACCAAGGCGACCTGTGTGAGGTGTGTGATGACCTGGAATCAAGGGAGAAATGCCAGAGCT	2340
QY	2580	CACCAAGACTTGGGCGAGCTCTCTCTGACAAAGCTGTGTTCTCTTGTGGTTTGGAGGAAGCA	2639
Db	2341	CACCAAGACTTGGGCGAGCTCTCTCTGACAAAGCTGTGTTCTCTTGTGGTTTGGAGGAAGCA	2400
QY	2640	ATGCAAGCTGGGCTGGGTGTATGCTCTCTCCCGCCCAAGGTGACATGAGTACAGACCTCTC	2699
Db	2401	ATGCAAGCTGGGCTGGGTGTATGCTCTCTCCCGCCCAAGGTGACATGAGTACAGACCTCTC	2460
QY	2700	TCAATACCAACATTTGAGCTCTGTCTTTTGGGGGTGCGCTGCTCCAGAGAGACCCCAAC	2759
Db	2461	TCAATACCAACATTTGAGCTCTGTCTTTTGGGGGTGCGCTGCTCCAGAGAGACCCCAAC	2520
QY	2760	ATTCACTGTGACATCTTTCCGTGACACCTGCTGAAAGAGGTCTGGTGGGAGAGCCAG	2819
Db	2521	ATTCACTGTGACATCTTTCCGTGACACCTGCTGAAAGAGGTCTGGTGGGAGAGCCAG	2580
QY	2820	TTCCCATAGGAAGGATCTGCC 2841	
Db	2581	TTCCCATAGGAAGGATCTGCC 2602	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 16:34:27 ; Search time 74 Seconds  
(Without alignments)  
3096.568 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQLGLAGSNMVEYKRA.....RHFGCPVSGPMNPGQICEW 811

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4281	100.0	811	6 ABG76487	Abg76487 Human zin
2	3982.5	93.0	756	6 AAU92722	Aau92722 Amino aci
3	3824.5	89.3	736	2 AAY41774	Aay41774 Human PRO
4	3824.5	89.3	736	3 AAB44330	Aab44330 Human PRO
5	3824.5	89.3	736	4 AAU92923	Aau92923 Human PRO
6	3824.5	89.3	736	6 ABUS8609	Abus8609 Human PRO
7	3824.5	89.3	736	6 ABUS8157	Abus8157 Novel hum
8	3824.5	89.3	736	6 ABUS94472	Abus94472 Human sec
9	3824.5	89.3	736	6 ABR65346	Abri65346 Human sec
10	3824.5	89.3	736	6 ABR65736	Abri65736 Human sec
11	3824.5	89.3	736	6 ABUS9676	Abus9676 Human sec
12	3824.5	89.3	736	6 ABUS2915	Abus2915 Human PRO
13	3824.5	89.3	736	6 ABUS9036	Abus9036 Novel hum
14	3824.5	89.3	736	6 ABR68285	Abri68285 Human sec
15	3824.5	89.3	736	6 ABUS6338	Abus6338 Novel hum
16	3824.5	89.3	736	6 ABUS2769	Abus2769 Human sec
17	3824.5	89.3	736	6 ABO08846	Abou08846 Human sec
18	3824.5	89.3	736	6 ABO02898	Abou02898 Human sec
19	3824.5	89.3	736	6 ABR75052	Abri75052 Human sec
20	3824.5	89.3	736	6 ABR94814	Abri94814 Human sec
21	3824.5	89.3	736	6 ABO25276	Abou25276 Novel hum
22	3824.5	89.3	736	6 ABUS5787	Abus5787 Human PRO
23	3824.5	89.3	736	6 ABUS9947	Abus9947 Novel hum
24	3824.5	89.3	736	6 ABUS9162	Abus9162 Novel hum
25	3824.5	89.3	736	6 ABUS1868	Abus1868 Novel hum

#### ALIGNMENTS

RESULT 1	ABG76487	standard; protein, 811 AA.
ID	ABG76487;	
AC	ABG76487;	
XX		
XX	12-MAY-2003 (first entry)	
DE	Human zinc metalloprotease.	
XX		
KW	Human; enzyme; zinc metalloprotease; metastatic cancer; tumour;	
KW	osteoarthritis; rheumatoid arthritis; septic arthritis;	
KW	peridontal disease; corneal ulceration; proteinuria;	
KW	coronary thrombosis; aneurysm aortic disease; birth control;	
KW	dyctrophic epidermolysis bullosa; degenerative cartilage loss;	
KW	inflammatory response; osteopaenia; tempo mandibular joint disease;	
KW	nervous system demyelinating disease; chromosome 3.	
OS	Homo sapiens.	
XX		
PN	US6482629-B1.	
XX		
PD	19-NOV-2002.	
XX		
PF	29-MAR-2001, 2001US-00819989.	
XX		
PR	29-MAR-2001, 2001US-00819989.	
XX		
PA	(APPL-) APPLERA CORP.	
PI		
XX		
PI	Wei M, Yan C, Di Francesco V, Beasley EM;	
XX		
DR	WPI, 2003-298138/29.	
XX		
DR	N-PSDB; ABX13166, ABX13167.	
XX		
PT	New human zinc metalloprotease enzymes and nucleic acids encoding them,	
XX	useful as models in developing and identifying human therapeutics, or as	
PT	targets for developing therapeutic agents that modulate enzyme activity.	
XX		
PS	Claim 1, Fig 2, 49p; English.	
XX		
CC	The invention relates an isolated nucleic acid molecule (cDNA and gene)	
CC	comprising a sequence encoding a human zinc metalloprotease. Also	
CC	included are vectors and host cells for expression of the polypeptide.	
CC	The human zinc metalloprotease and nucleic acids encoding them are useful	
CC	as models in the development of human therapeutics, in the identification	
CC	of therapeutic proteins, as targets for the development of human	
CC	therapeutic agents that modulate enzyme activity in cells and tissues	

26	3824.5	89.3	736	6 ABU72282	Abu72282 Novel hum
27	3824.5	89.3	736	6 ABUS9561	Abus9561 Human PRO
28	3824.5	89.3	736	6 ABUS6402	Abus6402 Human sec
29	3824.5	89.3	736	6 ABUS7615	Abus7615 Human sec
30	3824.5	89.3	736	6 ABUS0643	Abus0643 Human PRO
31	3824.5	89.3	736	6 ABR99561	Abri99561 Human sec
32	3824.5	89.3	736	6 ABR98951	Abri98951 Human sec
33	3824.5	89.3	736	6 ABO16474	Abou16474 Human sec
34	3824.5	89.3	736	6 ABR92374	Abri92374 Human sec
35	3824.5	89.3	736	6 ABO19015	Abou19015 Human sec
36	3824.5	89.3	736	6 ABR78436	Abri78436 Human sec
37	3824.5	89.3	736	6 ABO05172	Abou05172 Novel hum
38	3824.5	89.3	736	6 ABO00311	Abou00311 Novel hum
39	3824.5	89.3	736	6 ABO11643	Abou11643 Human sec
40	3824.5	89.3	736	6 ABO02288	Abou02288 Human sec
41	3824.5	89.3	736	6 ABUS8862	Abus8862 Novel hum
42	3824.5	89.3	736	6 ABUS3557	Abus3557 Human sec
43	3824.5	89.3	736	6 ABO06358	Abou06358 Novel hum
44	3824.5	89.3	736	6 ABR59394	Abri59394 Human sec
45	3824.5	89.3	736	6 ABO09456	Abou09456 Human sec





Best Local Similarity 94.2%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 47; Gaps 2;

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DB 1 MNVALDELGAGNMVEYKATLTDEDAPEPTVEGASPDAME-----42
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DB 43 -----VFQKGTROLGSRQLDELVLGASILLAL 74
QY 121 LGLVALGVQYHRDPSTCTEACIRVAGKILLESIDRGVSPCEDFYQSCGMIRNPL 180
DB 75 LGLVALGVQYHRDPSTCTEACIRVAGKILLESIDRGVSPCEDFYQSCGMIRNPL 134
QY 181 PDGRSRMTFNSLMDONQAILKHLNNTNSSSEAEQKQRYFLSCLQYRIEELGAOP 240
DB 135 PDGRSRMTFNSLMDONQAILKHLNNTNSSSEAEQKQRYFLSCLQYRIEELGAOP 194
QY 241 LRDLIRKIGGWNITGPMDDNFMELKAVAGTRAPPTFYVYISAKSSNSNVIOVDOS 300
DB 195 LRDLIRKIGGWNITGPMDDNFMELKAVAGTRAPPTFYVYISAKSSNSNVIOVDOS 254
QY 301 GLFLPSRDYIANTANEKVLTAVIDYMEELGMLGGRPTSTRQMOQVLELEIOLANITV 360
DB 255 GLFLPSRDYIANTANEKVLTAVIDYMEELGMLGGRPTSTRQMOQVLELEIOLANITV 314
QY 361 PDQDRDEEKIYHKMSISELOALAPSMWMEFLSPLEISDESEVTVYGMIDYLOQVS 420
DB 315 PDQDRDEEKIYHKMSISELOALAPSMWMEFLSPLEISDESEVTVYGMIDYLOQVS 374
QY 421 ELINRTEPSILNNYILMNLVOKTSSLDREPSAEOELTELGTCKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNYILMNLVOKTSSLDREPSAEOELTELGTCKSCVPRMOTCISNT 434
QY 481 DDALGFALGSLFYKATFPDRQSKELAEQ-MISEIRTAPEEALGOLVWMDKTRQAAEKAD 539
DB 435 DDALGFALGSLFYKATFPDRQSKELAEQ-MISEIRTAPEEALGOLVWMDKTRQAAEKAD 494
QY 540 AIYDMIGFDPDILPEKELDVYDGYEISEDSFQNMNLNYSFAKWADQLRKPSPRDOW 599
DB 495 AIYDMIGFDPDILPEKELDVYDGYEISEDSFQNMNLNYSFAKWADQLRKPSPRDOW 554
QY 600 SMTPOVNAAYLLPTKNEIVPPAGILOAPFARHNPXKALNFGGIGVWGHETLTAFDQGR 659
DB 555 SMTPOVNAAYLLPTKNEIVPPAGILOAPFARHNPXKALNFGGIGVWGHETLTAFDQGR 614
QY 660 EYDKENLRPMQNESILAFRNHTACMEEOYNOYVNGERLNGRQTLGENIADNGGLKAA 719
DB 615 EYDKENLRPMQNESILAFRNHTACMEEOYNOYVNGERLNGRQTLGENIADNGGLKAA 674
QY 720 YNAAYKALRRHGEBOQLPAVGLTNHQLFVGFPAQWCVPTPSSHEGLVTDPHSPARFR 779
DB 675 YNAAYKALRRHGEBOQLPAVGLTNHQLFVGFPAQWCVPTPSSHEGLVTDPHSPARFR 734
QY 780 VLGTLNSRDLRHHFGCPVGSPPMNPQQLCEW 811
DB 735 VLGTLNSRDLRHHFGCPVGSPPMNPQQLCEW 766
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## RESULT 3

AA41774  
AA41774 standard; protein; 736 AA.

XX  
AA41774;

DT 07-DEC-1999 (first entry)

DE Human PRO403 protein sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;

KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;

KW secreted protein; transmembrane protein.

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XX OS Homo sapiens.
XX PN W09946281-A2.
XX PD 16-SEP-1999.
XX PF 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 12-MAR-1998; 98US-0077649P.
XX 13-MAR-1998; 98US-0077791P.
XX 17-MAR-1998; 98US-00040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078936P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
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XX 31-MAR-1998; 98US-0080105P.
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XX 31-MAR-1998; 98US-0080165P.
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XX 01-APR-1998; 98US-0080327P.
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XX 08-APR-1998; 98US-0081049P.
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XX 09-APR-1998; 98US-0081195P.
XX 09-APR-1998; 98US-0081203P.
XX 09-APR-1998; 98US-0081229P.
XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081838P.
XX 15-APR-1998; 98US-0081952P.
XX 15-APR-1998; 98US-0081955P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082804P.
XX 23-APR-1998; 98US-0082767P.
XX 23-APR-1998; 98US-0082796P.
XX 27-APR-1998; 98US-0083336P.
XX 28-APR-1998; 98US-0083322P.
XX 28-APR-1998; 98US-0083392P.
XX 29-APR-1998; 98US-0083495P.
XX 29-APR-1998; 98US-0083496P.
XX 29-APR-1998; 98US-0083499P.
XX 29-APR-1998; 98US-0083500P.
XX 29-APR-1998; 98US-0083545P.
XX 29-APR-1998; 98US-0083554P.
XX 29-APR-1998; 98US-0083558P.
XX 29-APR-1998; 98US-0083559P.
XX 30-APR-1998; 98US-0083742P.
XX 05-MAY-1998; 98US-0084366P.
XX 06-MAY-1998; 98US-0084414P.
XX 06-MAY-1998; 98US-0084416P.
XX 07-MAY-1998; 98US-0084598P.
XX 07-MAY-1998; 98US-0084600P.
XX 07-MAY-1998; 98US-0084627P.
XX 07-MAY-1998; 98US-0084637P.
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PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085333P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086332P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR MPI; 1999-551358/46.
XX
DR N-PSDB; AA234326.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS Claim 12; Fig 225; 530p; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA241685 to
CC AA241774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
XX Sequence 736 AA;
SQ
Query Match 89.3%; Score 3824.5; DB 2; Length 736;
Best Local Similarity 99.9%; Pred. No. 1.2e-307;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 89 VGFQKGRQLGSTRQLELVLAGASLLALLLGCVLVGVYHRDPSHSTCTBACTIRV 148
DB 14 VGFQKGRQLGSTRQLELVLAGASLLALLLGCVLVGVYHRDPSHSTCTBACTIRV 73
QY 149 AGKILSLDRGVSPCEDFYQFSCGWRIRNPLPDGSRMTFTSLMDONAILKHLENT 208
DB 74 AGKILSLDRGVSPCEDFYQFSCGWRIRNPLPDGSRMTFTSLMDONAILKHLENT 133
QY 209 TENSSTSAEOKTORFYISCIQVERIEELGAQPLDLIEKIGWNITGPMQDNFMETLKA 268
DB 134 TENSSTSAEOKTORFYISCIQVERIEELGAQPLDLIEKIGWNITGPMQDNFMETLKA 193
QY 269 VAGTYRATPEFTFYISDSKSSNSNVQVOSGLFLPSRYIYNRTANEVLTAYLDYME 338
DB 194 VAGTYRATPEFTFYISDSKSSNSNVQVOSGLFLPSRYIYNRTANEVLTAYLDYME 253
QY 329 ELGMLLGRPTSTREQMOQVLELEIQLANITVPOQDRDEKITYHKMISIELQALAPSM 388

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DB 254 ELGMLLGRPTSTREQMOQVLELEIQLANITVPOQDRDEKITYHKMISIELQALAPSM 313
QY 389 WLEFLSFLSPLELSDSEPVVYGYNDYLOQVSELINRTPTSLINNYLTINLVOKTSSLD 448
DB 314 WLEFLSFLSPLELSDSEPVVYGYNDYLOQVSELINRTPTSLINNYLTINLVOKTSSLD 373
QY 449 RRPESAQELLETLYGTKKSCVPRMQTCISNTDDALGFALGSLFYVATPDROSKETAEQM 508
DB 374 RRPESAQELLETLYGTKKSCVPRMQTCISNTDDALGFALGSLFYVATPDROSKETAEQM 433
QY 509 ISEIRTAPEEALGQVWMDKTRQAKERADAIDYMGEPDILEPKELDVYGEISE 568
DB 434 ISEIRTAPEEALGQVWMDKTRQAKERADAIDYMGEPDILEPKELDVYGEISE 493
QY 569 DSFFQNMNLNYPASAKVADQLRKPPSRQMSMTQTVAAVYLPKNEIVPEAGLIQAF 628
DB 494 DSFFQNMNLNYPASAKVADQLRKPPSRQMSMTQTVAAVYLPKNEIVPEAGLIQAF 553
QY 629 YARNHPKALNPGGIGVVMGHELTAFDDQGREYDEKGNLRPMWONESLAFNNHTACME 688
DB 554 YARNHPKALNPGGIGVVMGHELTAFDDQGREYDEKGNLRPMWONESLAFNNHTACME 613
QY 689 QYNQYVNGERLNGRQTIGENTADNGGLKAAVNAAYKWLKKGEEQQLPAVGLTNHQLFF 748
DB 614 QYNQYVNGERLNGRQTIGENTADNGGLKAAVNAAYKWLKKGEEQQLPAVGLTNHQLFF 673
QY 749 VGFQVWCVRTPPESHEGLVTDPPSPAFRLTGLTSSNRDILRHGCVGSPMNPQQLC 808
DB 674 VGFQVWCVRTPPESHEGLVTDPPSPAFRLTGLTSSNRDILRHGCVGSPMNPQQLC 733
QY 809 EVW 811
DB 734 EVW 736
RESULT 4
AAB44330
ID AAB44330 standard; protein; 736 AA.
XX
AC AAB44330;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO403 protein sequence SEQ ID NO:526.
XX
KM Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US0005028.
PR 12-MAR-1999; 99US-0123857P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.

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PR 06-JAN-2000; 2000MO-US000376.  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,  
 PI Ferreira N, Filvaroff E, Fong S, Gao W, Geber H, Gerritsen ME,  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
 PI Kijavitt J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
 PI Stewart TA, Thomas D, Williams PM, Wood WI;  
 DR WPI; 2000-611443/58.  
 DR N-PSDB; AAC78592.  
 XX  
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
 PT target bioactive molecules to specific cells, and to modulate cellular  
 PT activities.  
 XX  
 XX Claim 12; Fig 225; 636pp; English.  
 PS  
 XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
 CC polynucleotides and polypeptides can be used for detecting the presence  
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
 CC and for modulating biological activities of cells, using the polypeptides  
 CC for specific targeting. The polypeptide targeting can be used to kill the  
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
 CC AAC78987 represent PCR primers and probes used in the isolation of the  
 CC PRO polynucleotide sequences  
 CC  
 XX  
 XX Sequence 736 AA:  
 SO  
 Query Match 89.3%; Score 3824.5; DB 3; Length 736;  
 Best Local Similarity 99.9%; Pred. No. 1.2e-307;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 629 YARNHFKALNFGSIGVGMGHELTAFDDQREYDKGNLRPMQNSLAAFRNHTACME 688  
 |||||  
 Db 554 YARNHFKALNFGSIGVGMGHELTAFDDQREYDKGNLRPMQNSLAAFRNHTACME 613  
 |||||  
 QY 689 QYNQYQVNGERLNGRQTLGENTADNGGLKAAVYAYAMLRKGEBOQLPAVGLTNHQLFF 748  
 |||||  
 Db 614 QYNQYQVNGERLNGRQTLGENTADNGGLKAAVYAYAMLRKGEBOQLPAVGLTNHQLFF 673  
 |||||  
 QY 749 VGFPAQVWCVSVPTESSHEGLVTDPPHSPARFRVLTGTSNSRDLRHFQCPVGSPPMNTGQLC 808  
 |||||  
 Db 674 VGFPAQVWCVSVPTESSHEGLVTDPPHSPARFRVLTGTSNSRDLRHFQCPVGSPPMNTGQLC 733  
 |||||  
 QY 809 EVM 811  
 |||||  
 Db 734 EVM 736  
 |||||  
 RESULT 5  
 ID AAU29233 standard; protein; 736 AA.  
 AAU29233  
 AC AAU29233;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #210.  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200168848-A2.  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001MO-US006520.  
 XX  
 PR 01-MAR-2000; 2000MO-US005601.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 06-MAR-2000; 2000US-0186968P.  
 PR 14-MAR-2000; 2000US-0189320P.  
 PR 14-MAR-2000; 2000US-0189328P.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000MO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000MO-US023328.  
PR 08-NOV-2000; 2000MO-US030952.  
PR 01-DEC-2000; 2000MO-US032678.  
PR 20-DEC-2000; 2000MO-US034956.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2001-602746/68.  
XX N-PSDB; AAS46134.  
DR Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.  
XX  
XX Claim 11; Fig 420; 774pp; English.  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumor in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumor in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumor necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumors and also  
CC susceptibility to tumor development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumors, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders  
XX  
XX Sequence 736 AA.  
Query Match 89.3%; Score 3824.5; DB 4; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1.2e-307;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 89 VGFQKGRQLLSGRTQELVLAGASILLALLGCVLAVQVHRDPSHSTCTEACIRV 148  
DB 14 VGFQKGRQLLSGRTQELVLAGASILLALLGCVLAVQVHRDPSHSTCTEACIRV 73  
QY 149 AGKILLESIDRGVSPCEDFYQFSCGWIIRNPLPDGRSRMNTFSLMDQNALIKHLENT 208  
DB 74 AGKILLESIDRGVSPCEDFYQFSCGWIIRNPLPDGRSRMNTFSLMDQNALIKHLENT 133  
QY 209 TENSSSAEOKTORFYLISCLQVERIEELGAQPLDLIEKIGWNITGPMQDNFMEYLKA 268  
DB 134 TENSSSAEOKTORFYLISCLQVERIEELGAQPLDLIEKIGWNITGPMQDNFMEYLKA 193  
QY 269 VAGTYRATPEFTYVYISADSKSSNSNVQVDSGLFLPSRYLYNRTNEKVLTRAYLDYME 338  
DB 194 VAGTYRATPEFTYVYISADSKSSNSNVQVDSGLFLPSRYLYNRTNEKVLTRAYLDYME 253  
QY 329 ELGMLLGRPTSTREQOQVLELEIQLANITVPDQRRDEKITYHKMSISELQALAPSM 388  
DB 254 ELGMLLGRPTSTREQOQVLELEIQLANITVPDQRRDEKITYHKMSISELQALAPSM 313  
QY 389 WLEPLSLPLSLSDSEPVVYTGMDYLQOVSELIINFTEPSLIANNLYINLVQKTTSSLD 448  
DB 314 WLEPLSLPLSLSDSEPVVYTGMDYLQOVSELIINFTEPSLIANNLYINLVQKTTSSLD 373  
QY 449 RRESAEOEKLLETLTGKKSQVPMWOCISNTDDAGFAGSLFVKATPPROSKETAEEM 508  
DB 374 RRESAEOEKLLETLTGKKSQVPMWOCISNTDDAGFAGSLFVKATPPROSKETAEEM 433  
QY 509 ISEIRTAFFBALGQLVMDEKTRQAAKEKADAIYDMIGPDPFLPEKELDDVYDGEISE 568

DB 434 ISEIRTAFFBALGQLVMDEKTRQAAKEKADAIYDMIGPDPFLPEKELDDVYDGEISE 493  
QY 569 DSEFQNMNLNYPASAWADQLRKPPSRQMSMTPTQVNAAYLLPTNNEIVFPAGLIQAPF 628  
DB 494 DSEFQNMNLNYPASAWADQLRKPPSRQMSMTPTQVNAAYLLPTNNEIVFPAGLIQAPF 553  
QY 629 YARNHPKALNPGIGVWVGHETLTHAFDDGREYDKEGNLRPMWONESLAFRNHTACME 688  
DB 554 YARNHPKALNPGIGVWVGHETLTHAFDDGREYDKEGNLRPMWONESLAFRNHTACME 613  
QY 689 QYNQYQVNERLNGRQTIGENIADNGLKAAYNAAYKWLKXGEEQQLPAVGLTNHQLFF 748  
DB 614 QYNQYQVNERLNGRQTIGENIADNGLKAAYNAAYKWLKXGEEQQLPAVGLTNHQLFF 673  
QY 749 VGFQVWCVRTPRESSHEGLVTDPHSPAFRVLGTLNSRDRLRHGCPVSPMNGQLC 808  
DB 674 VGFQVWCVRTPRESSHEGLVTDPHSPAFRVLGTLNSRDRLRHGCPVSPMNGQLC 733  
QY 809 EYW 811  
DB 734 EYW 736  
RESULT 6  
ID ABUS6609 standard; protein; 736 AA.  
XX ABUS6609;  
AC 15-APR-2003 (first entry)  
DT Human PRO polypeptide #210.  
XX DE Human PRO polypeptide #210.  
XX KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;  
XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;  
XX antibody-dependent enzyme mediated prodrug therapy.  
XX OS Homo sapiens.  
XX UN US2003027272-A1.  
XX PD 06-FEB-2003.  
XX PF 21-JUN-2002; 2002US-00176492.  
XX 18-SEP-1997; 97US-0059263P.  
XX 18-SEP-1997; 97US-0059266P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 21-OCT-1997; 97US-0063486P.  
XX 24-OCT-1997; 97US-0063120P.  
XX 24-OCT-1997; 97US-0063121P.  
XX 28-OCT-1997; 97US-0063540P.  
XX 28-OCT-1997; 97US-0063541P.  
XX 28-OCT-1997; 97US-0063544P.  
XX 28-OCT-1997; 97US-0063564P.  
XX 29-OCT-1997; 97US-0063734P.  
XX 31-OCT-1997; 97US-0063870P.  
XX 31-OCT-1997; 97US-0064103P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 21-NOV-1997; 97US-0066121P.  
XX 24-NOV-1997; 97US-0066466P.  
XX 24-NOV-1997; 97US-0066772P.  
XX 11-DEC-1997; 97US-0069335P.  
XX 12-DEC-1997; 97US-0069425P.  
XX 17-DEC-1997; 97US-0069870P.  
XX 18-DEC-1997; 97US-0068017P.  
XX 10-MAR-1998; 98US-0077450P.  
XX 11-MAR-1998; 98US-0077632P.  
XX 11-MAR-1998; 98US-0077649P.  
XX 20-MAR-1998; 98US-0078886P.  
XX 20-MAR-1998; 98US-0078939P.  
XX 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 01-APR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081043P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082777P.  
PR 28-APR-1998; 98US-0083322P.  
PR 28-APR-1998; 98US-0083455P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083559P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086033P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 03-JUN-1998; 98US-0087759P.  
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PR 04-JUN-1998; 98US-0088039P.  
PR 04-JUN-1998; 98US-0088033P.  
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PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 11-JUN-1998; 98US-0088866P.  
PR 12-JUN-1998; 98US-0088909P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089515P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089589P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089952P.  
PR 22-JUN-1998; 98US-0090246P.  
PR 22-JUN-1998; 98US-0090252P.  
PR 22-JUN-1998; 98US-0090254P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090435P.  
PR 24-JUN-1998; 98US-0090444P.  
PR 24-JUN-1998; 98US-0090461P.  
PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
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PR 07-OCT-1998; 98US-00168978.

Query Match 89.3%; Score 3824.5; DB 6; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1.2e-307;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 149 AGKILSLDRGVSPCEDFYQPSCGWIRNPLPDGSRMNTFNSLMDONAILKHILENT 208  
DB 74 AGKILSLDRGVSPCEDFYQPSCGWIRNPLPDGSRMNTFNSLMDONAILKHILENT 133  
QY 209 TPNSSSAEOKTQAFYISCIQVERIEELGAPLDLEKIGMNTTGPMDQDMFETLKA 268  
DB 134 TPNSSSAEOKTQAFYISCIQVERIEELGAPLDLEKIGMNTTGPMDQDMFETLKA 193  
QY 269 VAGTYRATPEFTYISADSKSNSNVTQVDSGLFLPSRDYILNRANKVLTAYLDYME 328  
DB 194 VAGTYRATPEFTYISADSKSNSNVTQVDSGLFLPSRDYILNRANKVLTAYLDYME 253  
QY 329 ELGMLLGRPTSTREMOQVLELEIQLANITVPDQDRDEKIVHNSISELOALABSD 388  
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QY 389 WLEFLSLSLPLEISDSEPPVYVGMVLYQVSELIINTEPSIINNYILNVLNOKTSSLD 448  
DB 314 WLEFLSLSLPLEISDSEPPVYVGMVLYQVSELIINTEPSIINNYILNVLNOKTSSLD 373  
QY 449 RREPSAOKLELLETLYGFKSCVPRMOTCIENITDIALGALSLFVKATPDROSKELAEQM 508  
DB 374 RREPSAOKLELLETLYGFKSCVPRMOTCIENITDIALGALSLFVKATPDROSKELAEQM 433  
QY 509 ISEIRTAFFEBALGQVMMDEKTRQAAKEKADAIYDMIGPPDFILPEPELDDVYDYEISE 568  
DB 434 ISEIRTAFFEBALGQVMMDEKTRQAAKEKADAIYDMIGPPDFILPEPELDDVYDYEISE 493  
QY 569 DSFFQNNMLNYSFAKVMADQLRKRPSRDQMSMTPTQVNAVYLLPTKNEIVFPAGILQAPF 628  
DB 494 DSFFQNNMLNYSFAKVMADQLRKRPSRDQMSMTPTQVNAVYLLPTKNEIVFPAGILQAPF 553  
QY 629 YARNHPKALNFGGIGVVMGHELTTHAFDDQGREYDKENLRPMQNESIAAFRNHTACME 688  
DB 554 YARNHPKALNFGGIGVVMGHELTTHAFDDQGREYDKENLRPMQNESIAAFRNHTACME 613  
QY 689 QYNQYQVNGERLNGRQTLGENIADNGGLKAAVNAKMLRKHGEEQLPAVGLTNTQLFF 748  
DB 614 QYNQYQVNGERLNGRQTLGENIADNGGLKAAVNAKMLRKHGEEQLPAVGLTNTQLFF 673  
QY 749 VGFQVWCSVRTPRESSHEGLVTDPHSPARPRVLTLSNSDPLAHRCPCVSPNPOQLC 808  
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AC ABU88157;  
XX  
DT 07-JUL-2003 (first entry)  
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DE Novel human secreted and transmembrane protein PRO740.

XX Human; secreted and transmembrane protein; PRO; gene therapy;  
KW tumour necrosis factor-alpha release; TNF-alpha release;  
KW chondrocyte proliferation; chondrocyte differentiation; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX Homo sapiens.

XX US2003032127-A1.

XX 13-FEB-2003.

XX 26-JUN-2002; 2002US-00183012.

XX 18-SEP-1997; 97US-0059263P.  
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Query Match 89.3%; Score 3824.5; DB 6; Length 736;
Best Local Similarity 99.9%; Pred. No. 1,2e-307;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 149 AGKILESILDRGVSPCEDFYQFSCGGMIRNPNLPDGRSRNNTNSLWDONQAIKHLENT 208
DB 74 AGKILESILDRGVSPCEDFYQFSCGGMIRNPNLPDGRSRNNTNSLWDONQAIKHLENT 133
QY 209 TENSSSEABOKTORFLSLCLOVERIEELGAOPRLDIEKIGMNITGPMDDONPMELVLA 268
DB 134 TENSSSEABOKTORFLSLCLOVERIEELGAOPRLDIEKIGMNITGPMDDONPMELVLA 193
QY 269 VAGTYRATPEFTYVYISADSKSSNSVYIQVDSGLFLPSRDYVYLNFTANEKVLTAAYDYNE 328
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PR 07-OCT-1998; 98US-00168978.  
  
Query Match 89.3%; Score 3824.5; DB 6; Length 736;  
Best Local Similarity 99.9%; Pred. No. 1,2e-107;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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QY 149 AGKILESILRGVSPCSDPYOFGCGWIRRNPLPDGSRNNTFNSLMDONQALIKHLENT 208  
DB 74 AGKILESILRGVSPCSDPYOFGCGWIRRNPLPDGSRNNTFNSLMDONQALIKHLENT 133  
  
QY 209 TFNSSEAEOKTORFYLSCLOVERIEBELGAOPLRDLIERIGWNITGPMDDONFMEVLKA 268  
DB 134 TFNSSEAEOKTORFYLSCLOVERIEBELGAOPLRDLIERIGWNITGPMDDONFMEVLKA 193  
  
QY 269 VAGTYRATPFYIYISADSKSSNSNTIYVDOSGLFPLSPDYILNRPANEKVTATYIDYNE 328  
DB 194 VAGTYRATPFYIYISADSKSSNSNTIYVDOSGLFPLSPDYILNRPANEKVTATYIDYNE 253  
  
QY 329 ELGMLIGRPTSTRBMOOVLELEIOLANITVPODORRDEKIYHKMSISELOALPSMD 388  
DB 254 ELGMLIGRPTSTRBMOOVLELEIOLANITVPODORRDEKIYHKMSISELOALPSMD 313  
  
QY 389 WLEFLSFLSPLELSDBEPVVVYGM DYLOQVSELINRTEPSILNNYLNLYOKTSSLD 448  
DB 314 WLEFLSFLSPLELSDBEPVVVYGM DYLOQVSELINRTEPSILNNYLNLYOKTSSLD 373  
  
QY 449 RRFESAQEKLETLTYGTTKSCVPRWOTCISNTDDALGFALGSLFYKATPDROSKETIAEGM 508  
DB 374 RRFESAQEKLETLTYGTTKSCVPRWOTCISNTDDALGFALGSLFYKATPDROSKETIAEGM 433  
  
QY 509 ISEIRTAFFREALGOLVMMDEKTRQAKERADAIYDMIGFPDPILEPKELDVYDGYEIEB 568  
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QY 569 DSFFQNMNLNLYNFSAKVMADOLRKPPSRDOMSMTPTVNAAYLLPTNGEIVFPAGIQAPF 628  
DB 494 DSFFQNMNLNLYNFSAKVMADOLRKPPSRDOMSMTPTVNAAYLLPTNGEIVFPAGIQAPF 553  
  
QY 629 YARNHPKALNPGGIGVVMGHEILTHAFDDGREGYDKEGNIRPMMQNESLAFRNHTACMBE 688  
DB 554 YARNHPKALNPGGIGVVMGHEILTHAFDDGREGYDKEGNIRPMMQNESLAFRNHTACMBE 613  
  
QY 689 QYNQOVNGERLNGQTLGENTADNGGLKAAANAKAMRKKEBGOULPAVGLTNNQLFF 748  
DB 614 QYNQOVNGERLNGQTLGENTADNGGLKAAANAKAMRKKEBGOULPAVGLTNNQLFF 673  
  
QY 749 VGFPAQVWCVRTPESHSHEGLVTDPHSPARFRVLTGILSNSRDLFRHFGCVGSPMNGQLC 808  
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QY 809 EVW 811  
DB 734 EVW 736

RESULT 9  
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AC ABR66346;  
XX  
DT 05-AUG-2003 (first entry)  
XX  
DE Human secreted polypeptide PRO740, SEQ ID NO:420.  
XX  
XX Human; PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumor necrosis factor-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
XX antiarthritic; vulnery; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027278-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176987.  
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PR 01-OCT-1998; 98US-0102687P.

Query Match      89.3%; Score 3824.5; DB 6; Length 736;
Best Local Similarity 99.9%; Pred. No. 1.2e-307;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 194 VAGTYRATPFTVYISADSKSSNSNVIQVDSGLFLPSRDYILNRTANEKVLTAAYLDYME 253
QY 329 ELGMLIGRPSTSTREQMOQVLELEIQLANITVPQDRDEDEKIYHMSISELQALAPSD 388
DB 254 ELGMLIGRPSTSTREQMOQVLELEIQLANITVPQDRDEDEKIYHMSISELQALAPSD 313
QY 389 WLEFLSFLSPLELSDSEPVVYVYGYDYLQVSELNRTPTSLNNTLYLNLYQKTTSSLD 448
DB 314 WLEFLSFLSPLELSDSEPVVYVYGYDYLQVSELNRTPTSLNNTLYLNLYQKTTSSLD 373
QY 449 RRPESAOEKLLETLYGTGKSCVPRMOTCSINTDDALGFALGSLFYVATPDROSKEIAEGM 508
DB 374 RRPESAOEKLLETLYGTGKSCVPRMOTCSINTDDALGFALGSLFYVATPDROSKEIAEGM 433
QY 509 ISEIRTAPEEALGQVWMDKTRQAKAKADAIYDMIGFPDFILBPKELDYYDGEISE 568
DB 434 ISEIRTAPEEALGQVWMDKTRQAKAKADAIYDMIGFPDFILBPKELDYYDGEISE 493
QY 569 DSEFQWMLNLYNPSAKVWADQIRKPPSRDQMSNTPTQVNAAYLPTKNEIVFPAGILQAPF 628
DB 494 DSEFQWMLNLYNPSAKVWADQIRKPPSRDQMSNTPTQVNAAYLPTKNEIVFPAGILQAPF 553
QY 629 YARNHPKALNPGIGVWVGHETLTHAFDDGREYDKGNLRPMWONESLAPRNHTACME 688
DB 554 YARNHPKALNPGIGVWVGHETLTHAFDDGREYDKGNLRPMWONESLAPRNHTACME 613
QY 689 QYNQYVNGERLNGRQTLGENTADNGGLKAAVNAKWKAKGEEQQLPAVGLTNHQLFF 748
DB 614 QYNQYVNGERLNGRQTLGENTADNGGLKAAVNAKWKAKGEEQQLPAVGLTNHQLFF 673
QY 749 VGFQVWCVKRTPESSHEGLVTDPHSPAFRLVGLTSLNSRDILRHGCVGSPMNPGLC 808
DB 674 VGFQVWCVKRTPESSHEGLVTDPHSPAFRLVGLTSLNSRDILRHGCVGSPMNPGLC 733
QY 809 EYM 811
DB 734 EYM 736

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AC
XX
XX
DT 05-AUG-2003 (first entry)
XX
XX Human secreted polypeptide PRO740, SEQ ID NO:420.
DE
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnerary; gene therapy.
OS Homo sapiens.
XX
XX
XX US2003036159-A1.
XX
XX
XX 20-FEB-2003.
XX
XX
XX 02-JUL-2002; 2002US-00188773.
XX
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XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.

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Query Match 89.3%; Score 3824.5; DB 6; Length 736;
Best Local Similarity 99.9%; Pred. No. 1.2e-307;
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1674 VGFPAQVWCVRTPPESSHEGLVTDPHSPARFVLTGLTNSRDYLRHFGCPVGSPPMNGQLC 733
QY 809 EYW 811
DB 734 EYW 736

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AC ABU99676;
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DT 09-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #210.
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KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tissue necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003040070-A1.
XX
PD 27-FEB-2003.
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PF 27-JUN-2002; 2002US-00184627.
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Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KW Chondrocyte differentiation; tumour necrosis factor-alpha release;  
KW affinity purification.  
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KW chondrocyte; proliferation; differentiation; cartilage disorder;



KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 19:42:36 ; Search time 22 Seconds  
(without alignments)  
1903.121 Million cell updates/sec

Title: US-10-681-222-2

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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27	120	2.8	1192	4	US-09-134-000C-4844

28	118.5	2.8	825	4	US-09-489-039A-11003	Sequence 11003, A
29	116.5	2.7	703	4	US-09-308-345A-49	Sequence 49, Appl
30	115	2.7	2860	2	US-08-826-267-2	Sequence 2, Appl
31	114	2.7	1175	2	US-08-598-305A-36	Sequence 36, Appl
32	114	2.7	1175	2	US-08-639-923A-36	Sequence 36, Appl
33	113.5	2.7	1179	6	5188960-2	Patent No. 5188960
34	112	2.6	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
35	111.5	2.6	456	4	US-09-800-170-15	Sequence 15, Ap
36	110.5	2.6	818	4	US-09-134-000C-6355	Sequence 6355, Ap
37	110.5	2.6	1315	4	US-09-200-650B-5	Sequence 5, Appl
38	110.5	2.6	1493	4	US-09-489-039A-13687	Sequence 13687, A
39	109.5	2.6	703	3	US-09-422-869-27	Sequence 27, Appl
40	109.5	2.6	1093	5	PCT-US93-03077-1	Sequence 1, Appl
41	109.5	2.6	3635	4	US-09-845-583A-2	Sequence 2, Appl
42	108.5	2.5	3672	2	US-08-822-445-12	Sequence 12, Appl
43	108.5	2.5	3672	2	US-09-196-540-12	Sequence 12, Appl
44	108.5	2.5	3801	2	US-08-822-445-10	Sequence 10, Appl
45	108.5	2.5	3801	4	US-09-396-540-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1									
US-09-819-989-2									
; Sequence 2, Application US/0981989;									
; Patent No. 6482629									
; GENERAL INFORMATION:									
; APPLICANT: WEI, Ming-Hui et al.									
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC									
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES									
; TITLE OF INVENTION: THEREOF									
; FILE REFERENCE: CL001200									
; CURRENT APPLICATION NUMBER: US/09/819,989									
; CURRENT FILING DATE: 2001-03-29									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 811									
; TYPE: PRT									
; ORGANISM: Human									
; US-09-819-989-2									
Query Match									
Best Local Similarity 100.0%; Score 4281; DB 4; Length 811;									
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MNAVALQELGAGSNMVEYKRA	1	1	1	1	1	1	1
DB	1	MNAVALQELGAGSNMVEYKRA	1	1	1	1	1	1	1
QY	61	GTPRSSGLTWRVTCPLKRSISGLCSRTWVGFOKTRQLLSGRTOLELVLAGSLLAALL	61	61	61	61	61	61	61
DB	61	GTPRSSGLTWRVTCPLKRSISGLCSRTWVGFOKTRQLLSGRTOLELVLAGSLLAALL	61	61	61	61	61	61	61
QY	121	LGGLVAVGYVRHDSHTCLTEACRVAVKLIESIDRGVSPCEDFPYPSGCGMIRNPL	121	121	121	121	121	121	121
DB	121	LGGLVAVGYVRHDSHTCLTEACRVAVKLIESIDRGVSPCEDFPYPSGCGMIRNPL	121	121	121	121	121	121	121
QY	181	PDGRSMNTPNSLMDONQAILKHLLENTTFFNSSSEAEOKTORFYSCLQVERIEELGAOP	181	181	181	181	181	181	181
DB	181	PDGRSMNTPNSLMDONQAILKHLLENTTFFNSSSEAEOKTORFYSCLQVERIEELGAOP	181	181	181	181	181	181	181
QY	241	LRLDLIKIGKWNITGWDONFMEVUKAVAGYRATPFTVYISADSKSNSNVIOVDOS	241	241	241	241	241	241	241
DB	241	LRLDLIKIGKWNITGWDONFMEVUKAVAGYRATPFTVYISADSKSNSNVIOVDOS	241	241	241	241	241	241	241
QY	301	GLFLPSRDYILNRTANEKYLTVLIDYMEELGMLGGRPSTREBQOVLELQIANITY	301	301	301	301	301	301	301
DB	301	GLFLPSRDYILNRTANEKYLTVLIDYMEELGMLGGRPSTREBQOVLELQIANITY	301	301	301	301	301	301	301
QY	361	PDQDRDEKTIYHKISISELQALAPSMWLLEFLSLLELSDSEPVVYVGYMDYLOQVS	361	361	361	361	361	361	361
DB	361	PDQDRDEKTIYHKISISELQALAPSMWLLEFLSLLELSDSEPVVYVGYMDYLOQVS	361	361	361	361	361	361	361

Db 361 POPORDEEKIYHKMSISELOALAPSMWLEFLSLPLELSDSEPVVYVGYDQVS 420  
Qy 421 ELINRTEPSILNNYILNNVOKTSSLDRRPESAOEKLLETLYGTCKSCVPRMOTCISNT 480  
Db 421 ELINRTEPSILNNYILNNVOKTSSLDRRPESAOEKLLETLYGTCKSCVPRMOTCISNT 480  
Qy 481 DDALGFALSLFVKATFDOSKEIAEGMISEIRTAEEALGOLVMMDEKROAKKADA 540  
Db 481 DDALGFALSLFVKATFDOSKEIAEGMISEIRTAEEALGOLVMMDEKROAKKADA 540  
Qy 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSDQMS 600  
Db 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSDQMS 600  
Qy 601 MTPQTVNAYYLPKNEIVFPAGILQAPFYARHHPKALNFGIGVWGHETLTHAFDDQRE 660  
Db 601 MTPQTVNAYYLPKNEIVFPAGILQAPFYARHHPKALNFGIGVWGHETLTHAFDDQRE 660  
Qy 661 YDEKGNLRPMWQNESLAARNTACMEEOYNOYVNGEELNGRQTLGENIADNGLKAAY 720  
Db 661 YDEKGNLRPMWQNESLAARNTACMEEOYNOYVNGEELNGRQTLGENIADNGLKAAY 720  
Qy 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPSSHGLVTDPHSPARFV 780  
Db 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPSSHGLVTDPHSPARFV 780  
Qy 781 LGTLSNRDPLRHGCPVGSPPMNGQLCEW 811  
Db 781 LGTLSNRDPLRHGCPVGSPPMNGQLCEW 811

## RESULT 2

US-10-273-992-2  
; Sequence 2, Application US/10273992

; Patent No. 6664093  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001200DIV  
; CURRENT APPLICATION NUMBER: US/10/273,992  
; CURRENT FILING DATE: 2002-10-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Human  
US-10-273-992-2

Query Match 100.0%; Score 4281; DB 4; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEYVGKASPPSPGSPGMP 60  
Db 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEYVGKASPPSPGSPGMP 60  
Qy 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWGFQKGTROLLGSRTOLELVLAGASILLAAAL 120  
Db 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWGFQKGTROLLGSRTOLELVLAGASILLAAAL 120  
Qy 121 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFQFSCGWMIRNPL 180  
Db 121 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFQFSCGWMIRNPL 180  
Qy 181 PDGSRMNTFNSLMDONQALIKHLIENTTENSSEABOKTORFYLISLOVERIEEAGAP 240  
Db 181 PDGSRMNTFNSLMDONQALIKHLIENTTENSSEABOKTORFYLISLOVERIEEAGAP 240  
Qy 241 LRDLIEKIGGWNITGPMODNFMFEVLKAVAGYRATPEFTVYISADSKSNSNVYQVDS 300  
Db 241 LRDLIEKIGGWNITGPMODNFMFEVLKAVAGYRATPEFTVYISADSKSNSNVYQVDS 300

Db 241 LRDLIEKIGGWNITGPMODNFMFEVLKAVAGYRATPEFTVYISADSKSNSNVYQVDS 300  
Qy 301 GFLPSRDYVYLNNTAEKYLTAATDYMEELGMLGSRPSTEBOMQOVLELEIQLANITY 360  
Db 301 GFLPSRDYVYLNNTAEKYLTAATDYMEELGMLGSRPSTEBOMQOVLELEIQLANITY 360  
Qy 361 POPORDEEKIYHKMSISELOALAPSMWLEFLSLPLELSDSEPVVYVGYDQVS 420  
Db 361 POPORDEEKIYHKMSISELOALAPSMWLEFLSLPLELSDSEPVVYVGYDQVS 420  
Qy 421 ELINRTEPSILNNYILNNVOKTSSLDRRPESAOEKLLETLYGTCKSCVPRMOTCISNT 480  
Db 421 ELINRTEPSILNNYILNNVOKTSSLDRRPESAOEKLLETLYGTCKSCVPRMOTCISNT 480  
Qy 481 DDALGFALSLFVKATFDOSKEIAEGMISEIRTAEEALGOLVMMDEKROAKKADA 540  
Db 481 DDALGFALSLFVKATFDOSKEIAEGMISEIRTAEEALGOLVMMDEKROAKKADA 540  
Qy 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSDQMS 600  
Db 541 IYDMIGFPDPILEPKELDDVDYDGEISEDSFPQNMNLNFSKXVADQLRKPPSDQMS 600  
Qy 601 MTPQTVNAYYLPKNEIVFPAGILQAPFYARHHPKALNFGIGVWGHETLTHAFDDQRE 660  
Db 601 MTPQTVNAYYLPKNEIVFPAGILQAPFYARHHPKALNFGIGVWGHETLTHAFDDQRE 660  
Qy 661 YDEKGNLRPMWQNESLAARNTACMEEOYNOYVNGEELNGRQTLGENIADNGLKAAY 720  
Db 661 YDEKGNLRPMWQNESLAARNTACMEEOYNOYVNGEELNGRQTLGENIADNGLKAAY 720  
Qy 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPSSHGLVTDPHSPARFV 780  
Db 721 NAYKAMLRKHGEEOQLPAVGLTNHOLFVGFPAQVWCVRTPSSHGLVTDPHSPARFV 780  
Qy 781 LGTLSNRDPLRHGCPVGSPPMNGQLCEW 811  
Db 781 LGTLSNRDPLRHGCPVGSPPMNGQLCEW 811

## RESULT 3

US-09-819-989-4  
; Sequence 4, Application US/09819989

; Patent No. 6482629  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001200  
; CURRENT APPLICATION NUMBER: US/09/819,989  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Human  
US-09-819-989-4

Query Match 93.3%; Score 3993; DB 4; Length 765;  
Best Local Similarity 94.3%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

Qy 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEYVGKASPPSPGSPGMP 60  
Db 1 MNVALOELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEYVGKASPPSPGSPGMP 60  
Qy 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWGFQKGTROLLGSRTOLELVLAGASILLAAAL 120  
Db 61 GTPRSSGLFMRVTCPHLRISISGLCSRTWGFQKGTROLLGSRTOLELVLAGASILLAAAL 120  
Qy 43 -----VFQKGTROLLGSRTOLELVLAGASILLAAAL 74  
Db 43 -----VFQKGTROLLGSRTOLELVLAGASILLAAAL 74  
Qy 121 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFQFSCGWMIRNPL 180  
Db 121 LGCLVALGVQYHRDPSSHSTCLTEACIRVAGKILIESLDRGVSPCEDFQFSCGWMIRNPL 180



Db 75 LGCLVALGVQYHRDPSHSCTLEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 134  
QY 181 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 240  
Db 135 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 194  
QY 241 LRDLIEKIGGMNITGMPDQDNFMEVILKAVAGTYRATPFTVYISADSKSNSNVIOVDOS 300  
Db 195 LRDLIEKIGGMNITGMPDQDNFMEVILKAVAGTYRATPFTVYISADSKSNSNVIOVDOS 254  
QY 301 GLFLPSRDYILNRTANEKVTAYLDYMEBELGMLGGRPTSTREMOQVLELEIOLANITY 360  
Db 255 GLFLPSRDYILNRTANEKVTAYLDYMEBELGMLGGRPTSTREMOQVLELEIOLANITY 314  
QY 361 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 240  
Db 315 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 194  
QY 421 ELINRTEPSILNNYILNVLVQKTTSLDRPFESAQKLETLTYGKKSCVPRMOTCISNT 480  
Db 375 ELINRTEPSILNNYILNVLVQKTTSLDRPFESAQKLETLTYGKKSCVPRMOTCISNT 434  
QY 481 DDALGFALGSLFYKATFDROSKELIAGMISEIRTAPEALGOLVWMDKTRQAKAKADA 540  
Db 435 DDALGFALGSLFYKATFDROSKELIAGMISEIRTAPEALGOLVWMDKTRQAKAKADA 494  
QY 541 IYMGIFPDPFLEPKELADVDYDGEISEDSFQNMMLNLYNFSKAVADOLRKPSPRDOS 600  
Db 495 IYMGIFPDPFLEPKELADVDYDGEISEDSFQNMMLNLYNFSKAVADOLRKPSPRDOS 554  
QY 601 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARHNPKALNFGGIVVNGHELTHAFDQGRE 660  
Db 555 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARHNPKALNFGGIVVNGHELTHAFDQGRE 614  
QY 661 YDKEGNLRPMWQNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGGLKAA 720  
Db 615 YDKEGNLRPMWQNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGGLKAA 674  
QY 721 NAYKAWLRKHGEEQQLPAVGLTNHQLFVGFQAVWCVRTPSSSHEGLVTDPHSPARFRV 780  
Db 675 NAYKAWLRKHGEEQQLPAVGLTNHQLFVGFQAVWCVRTPSSSHEGLVTDPHSPARFRV 734  
QY 781 LGTILNSRDLRHFQCGVSPMNPQOLCEW 811  
Db 735 LGTILNSRDLRHFQCGVSPMNPQOLCEW 765

RESULT 4  
US-10-273-992-4  
; Sequence 4, Application US/10273992  
; Patent No. 6664093  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; FILE REFERENCE: C0001200D1V  
; CURRENT APPLICATION NUMBER: US/10/273,992  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Human  
US-10-273-992-4

Query Match 93.3%; Score 3993; DB 4; Length 765;  
Best Local Similarity 94.3%; Pred. No. 0;  
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

QY 1 MNVALQELGAGSNMVEYKRALTRDEDAPEPTVEGASPDAMEVGKASPPSPGSPGMP 60

Db 1 MNVALQELGAGSNMVEYKRALTRDEDAPEPTVEGASPDAMEVGKASPPSPGSPGMP 60  
QY 61 GTPRSSGLFWRVYCPHLRSISGLCSRTWVGFOKQTRQLGSRTOLEVLVAGASILLALL 120  
Db 43 -----VFQGRQLGSRTOLEVLVAGASILLALL 74  
QY 121 LGCLVALGVQYHRDPSHSCTLEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 180  
Db 75 LGCLVALGVQYHRDPSHSCTLEACIRVAGKILLESIDRGVSPCEDFYQFSCGGMIRRNPL 134  
QY 181 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 240  
Db 135 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 194  
QY 241 LRDLIEKIGGMNITGMPDQDNFMEVILKAVAGTYRATPFTVYISADSKSNSNVIOVDOS 300  
Db 195 LRDLIEKIGGMNITGMPDQDNFMEVILKAVAGTYRATPFTVYISADSKSNSNVIOVDOS 254  
QY 301 GLFLPSRDYILNRTANEKVTAYLDYMEBELGMLGGRPTSTREMOQVLELEIOLANITY 360  
Db 255 GLFLPSRDYILNRTANEKVTAYLDYMEBELGMLGGRPTSTREMOQVLELEIOLANITY 314  
QY 361 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 240  
Db 315 PDGRSWMNTFNSLMDONQAILKHLLENTFNSSSEABQKTOFPYLSCTLOYERIEBIGAOP 194  
QY 421 ELINRTEPSILNNYILNVLVQKTTSLDRPFESAQKLETLTYGKKSCVPRMOTCISNT 480  
Db 375 ELINRTEPSILNNYILNVLVQKTTSLDRPFESAQKLETLTYGKKSCVPRMOTCISNT 434  
QY 481 DDALGFALGSLFYKATFDROSKELIAGMISEIRTAPEALGOLVWMDKTRQAKAKADA 540  
Db 435 DDALGFALGSLFYKATFDROSKELIAGMISEIRTAPEALGOLVWMDKTRQAKAKADA 494  
QY 541 IYMGIFPDPFLEPKELADVDYDGEISEDSFQNMMLNLYNFSKAVADOLRKPSPRDOS 600  
Db 495 IYMGIFPDPFLEPKELADVDYDGEISEDSFQNMMLNLYNFSKAVADOLRKPSPRDOS 554  
QY 601 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARHNPKALNFGGIVVNGHELTHAFDQGRE 660  
Db 555 MPQOTNAVAYLLPKNEIVFPAGILQAPFYARHNPKALNFGGIVVNGHELTHAFDQGRE 614  
QY 661 YDKEGNLRPMWQNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGGLKAA 720  
Db 615 YDKEGNLRPMWQNESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGGLKAA 674  
QY 721 NAYKAWLRKHGEEQQLPAVGLTNHQLFVGFQAVWCVRTPSSSHEGLVTDPHSPARFRV 780  
Db 675 NAYKAWLRKHGEEQQLPAVGLTNHQLFVGFQAVWCVRTPSSSHEGLVTDPHSPARFRV 734  
QY 781 LGTILNSRDLRHFQCGVSPMNPQOLCEW 811  
Db 735 LGTILNSRDLRHFQCGVSPMNPQOLCEW 765

RESULT 5  
US-09-667-373-4  
; Sequence 4, Application US/09667373  
; Patent No. 6524840  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6524840el Human Endothelin Converting  
; TITLE OF INVENTION: Enzyme-Like Proteins and Polynucleotides Encoding the Same  
; FILE REFERENCE: IEX-0043-USA  
; CURRENT APPLICATION NUMBER: US/09/667,373  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US 60/156,102  
; PRIOR FILING DATE: 1999-09-24

PRIOR APPLICATION NUMBER: US 60/176,689  
PRIOR FILING DATE: 2000-01-18  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 883  
TYPE: PR  
ORGANISM: homo sapiens  
US-09-667-373-4

Query Match 89.2%; Score 3820; DB 4; Length 883;  
Best Local Similarity 97.8%; Pred. No. 0;  
Matches 726; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

70 WRYTCPLHSISGLCSRTWVGFGKTRQLGSRTOLELVLAGSLLAALLGCVAGV 129  
144 WTVSSECVHTVDVQLSE--VGFGKTRQLGSRTOLELVLAGSLLAALLGCVAGV 201  
130 QYHRDPESHSTCLTEACIRVAGKILSLDRGVSPCEDFYQSCGWIIRNPLPDGRSRMT 189  
202 QYHRDPESHSTCLTEACIRVAGKILSLDRGVSPCEDFYQSCGWIIRNPLPDGRSRMT 261  
190 FNSLMDQNAIILKHLLENTFNSSSEAEQKTRFYSLQVERIBELGAQPLDLIEKIG 249  
262 FNSLMDQNAIILKHLLENTFNSSSEAEQKTRFYSLQVERIBELGAQPLDLIEKIG 321  
250 GNNITGPMODNFMETLKAVAGTYRATPFTVYISADSKSNSNVIOVDOSGLFLPSRDY 309  
322 GNNITGPMODNFMETLKAVAGTYRATPFTVYISADSKSNSNVIOVDOSGLFLPSRDY 381  
310 YLNRTANEKYLTAVIDYMEELGMLGSRPTSTREOMQVLELEIOLANTITVPDORRDEE 369  
382 YLNRTANEKYLTAVIDYMEELGMLGSRPTSTREOMQVLELEIOLANTITVPDORRDEE 441  
370 KIYHKNSISELOALAPSMDWLEFLSLPLSLSDSEPPVYVGYMDYLOQVSELINRTEPS 429  
442 KIYHKNSISELOALAPSMDWLEFLSLPLSLSDSEPPVYVGYMDYLOQVSELINRTEPS 501  
430 ILNNYLIIMNVOKTSSLDLRRPESAOEKLLETLYGTGKSCVPRMOTCISNTDAGFALG 489  
502 ILNNYLIIMNVOKTSSLDLRRPESAOEKLLETLYGTGKSCVPRMOTCISNTDAGFALG 561  
490 SLFVKATFDRQSKELIAGMISEIRTAFEBAIGOLVWMDKTRQAAEKADAIYDMIGFDP 549  
562 SLFVKATFDRQSKELIAGMISEIRTAFEBAIGOLVWMDKTRQAAEKADAIYDMIGFDP 621  
550 FILEPEKELDVYDGYEISDSFPQNMNLNLYNSAKVADOLRKPERSDQMSMTPTQVNAV 609  
622 FILEPEKELDVYDGYEISDSFPQNMNLNLYNSAKVADOLRKPERSDQMSMTPTQVNAV 681  
610 YLPTKNIIVFPAGILQAPFYARNHPKALNFGGIGVNGHELTHAFDQGBREYDEGLRP 669  
682 YLPTKNIIVFPAGILQAPFYARNHPKALNFGGIGVNGHELTHAFDQGBREYDEGLRP 741  
670 WMQNESLAARNTACCEBOYNOYVNGERLNGRQTLGENTADNGGLKAAYNAKALARK 729  
742 WMQNESLAARNTACCEBOYNOYVNGERLNGRQTLGENTADNGGLKAAYNAKALARK 801  
730 HGEBOQLPAVGLTNHQLFVGFAGVWCVSVTPRESSHEGLVTPDPSPARFVLTLSNSRD 789  
802 HGEBOQLPAVGLTNHQLFVGFAGVWCVSVTPRESSHEGLVTPDPSPARFVLTLSNSRD 861  
QY 790 FLRHFGCPVGSPPMNPQOLCEVW 811  
DB 862 FLRHFGCPVGSPPMNPQOLCEVW 883

RESULT 6  
US-08-574-763-2  
Sequence 2, Application US/08574763  
Patent No. 5736376  
GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi

TITLE OF INVENTION: RECOMBINANT ENDOTHELIN CONVERTING  
TITLE OF INVENTION: ENZYME-2 AND ITS USE IN ECE INHIBITOR SCREENING  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: Concurrently herewith.  
APPLICATION NUMBER: US/08/574,763  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Cordier, Timothy S.  
REGISTRATION NUMBER: 38,414  
REFERENCE/DOCKET NUMBER: UTD:472  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 787 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-574-763-2

Query Match 85.5%; Score 3662; DB 1; Length 787;  
Best Local Similarity 93.0%; Pred. No. 0;  
Matches 690; Conservative 22; Mismatches 28; Indels 2; Gaps 1;

70 WRYTCPLHSISGLCSRTWVGFGKTRQLGSRTOLELVLAGSLLAALLGCVAGV 129  
48 WTVSSECVHTVDVQLSE--AGFRKTRSLGHTQLELVLAGSLLAALLGCVAGV 105  
130 QYHRDPESHSTCLTEACIRVAGKILSLDRGVSPCEDFYQSCGWIIRNPLPDGRSRMT 189  
106 QYHRDPESHSTCLTEACIRVAGKILSLDRGVSPCEDFYQSCGWIIRNPLPDGRSRMT 165  
190 FNSLMDQNAIILKHLLENTFNSSSEAEQKTRFYSLQVERIBELGAQPLDLIEKIG 249  
166 FNSLMDQNAIILKHLLENTFNSSSEAEQKTRFYSLQVERIBELGAQPLDLIEKIG 225  
250 GNNITGPMODNFMETLKAVAGTYRATPFTVYISADSKSNSNVIOVDOSGLFLPSRDY 309  
226 GNNITGPMODNFMETLKAVAGTYRATPFTVYISADSKSNSNVIOVDOSGLFLPSRDY 285  
310 YLNRTANEKYLTAVIDYMEELGMLGSRPTSTREOMQVLELEIOLANTITVPDORRDEE 369  
286 YLNRTANEKYLTAVIDYMEELGMLGSRPTSTREOMQVLELEIOLANTITVPDORRDEE 345  
370 KIYHKNSISELOALAPSMDWLEFLSLPLSLSDSEPPVYVGYMDYLOQVSELINRTEPS 429  
346 KIYHKNSISELOALAPSMDWLEFLSLPLSLSDSEPPVYVGYMDYLOQVSELINRTEPS 405  
430 ILNNYLIIMNVOKTSSLDLRRPESAOEKLLETLYGTGKSCVPRMOTCISNTDAGFALG 489  
406 ILNNYLIIMNVOKTSSLDLRRPESAOEKLLETLYGTGKSCVPRMOTCISNTDAGFALG 465  
490 SLFVKATFDRQSKELIAGMISEIRTAFEBAIGOLVWMDKTRQAAEKADAIYDMIGFDP 549  
466 SLFVKATFDRQSKELIAGMISEIRTAFEBAIGOLVWMDKTRQAAEKADAIYDMIGFDP 525  
550 FILEPEKELDVYDGYEISDSFPQNMNLNLYNSAKVADOLRKPERSDQMSMTPTQVNAV 609  
526 FILEPEKELDVYDGYEISDSFPQNMNLNLYNSAKVADOLRKPERSDQMSMTPTQVNAV 585

Qy	610	LLPFTNKEIVPAGILIOAEFYARNKHKPNFGIIGVWGHGELTHAPDDOREYDKGNLRP	669
Db	586	YLPFTNKEIVPAGILIOAEFYTCNMFQALNFGIIGVWGHGELTHAPDDOREYDKGNLRP	645
Qy	670	WMQNESLAEPNHTACMBEYOYNQYOVNGERLNGRQTIGENIADNGLKAAYNAYKAWLRX	729
Db	646	WMQNESLAEPNHTACTIEQYSQYOVNGERKLNGRQTIGENIADNGLKAAYNAYKAWLRX	705
Qy	730	HGEEOQLPAVGLTNHQLFYVFGPAQWCGSVRTPESHSEGLYNDPHSPARPRVLGITSNRD	789
Db	706	HGEEOQLPAVGLTNHQLFYVFGPAQWCGSVRTPESHSEGLYNDPHSPARPRVLGITSNRD	765
Qy	790	FLRFHGCVPVGSPPMNGOLCEWV	811
Db	766	FLRFHGCVPVGSPPMNSGOLCEWV	787

## RESULT 7

```

US-08-646-273-36
; Sequence 36, Application US/08646273
; Patent No. 6066502
;
GENERAL INFORMATION:
;
APPLICANT: Kroegeer, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
;
APPLICANT: Martin, Jacob, Elard, Oter, Rainer, Subkowski, Thomas, Hillen, Heinz
;
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE) .
;
NUMBER OF SEQUENCES: 36
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: Kell & Weinkauff
;
STREET: 1101 Connecticut Avenue
;
CITY: Washington
;
STATE: D.C.
;
COUNTRY: USA
;
ZIP: 20036
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
;
COMPUTER: IBM AT-compatible, 80486 processor
;
OPERATING SYSTEM: MS-DOS version 6.0
;
SOFTWARE: WordPerfect version 5.1
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/646,273
;
FILING DATE: 16-NOV-1994
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: PCT/EP94/03706
;
FILING DATE: 11-NOV-1994
;
INFORMATION FOR SEQ ID NO: 36:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 753 amino acids
;
TYPE: amino acid
;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
US-08-646-273-36

```

	Query Match	60.5%	Score 2590.5	DB 3	Length 753
	Best Local Similarity	60.1%	Pred. No. 6.8e-242		
	Matches 481	Conservative 122	Mismatches 148	Indels 49	Gaps 6
QY	14 MVEYKRAITLDEDAPEPTVPEGGAAPDAMEVGKASPFSPGSPSCMTGPTRPSGLFWRYT				73
Db	1 MSTYKRATLDEEDLVDSISGEDAYENGLQVNF-----HSPSGQRGW----				42
QY	74 CPHLRSSISGLCSRFMWGFQKKOTRQLLSGRTOLEVLNAGSLIATAALLIGCVALGGVOYH-				132
Db	43 -----AKRTVERKLVTLVLLNAGLVACLAALGIQTQT				76
QY	133 RDPESHSTCTEACIRVACKILIESLDRGVSPOCEDFQFSQCGMIRNPPLPDRSRSMTPNS				192
Db	77 RSP--SVCLSEACYSVTSSIIISMDPTVPDCHDFPSYACGMKANFVPDGHSRWGTFTSN				134
QY	193 LMDONAILKRLIENTTNSSSEAAOKTORLYTLCTOYERIEELGAQPLRLRIEKIGMN				252
Db	135 LMENNQAIIKRLINNST-AVSEAEARKAQVYRRCAEMETRIEELRAKIMLEIRLGAWN				193

QY	255	ITPEMOQDNFMEYLKAYAGATYATAPFPFYVYISAPSKSNSNVIVODSGFLPSRDYYLN	31.2
Db	194	ITPEWAKMDNFODILOVYVYAHYATSPFYSVYASBSKNSNVIVODSGFLPSRDYYLN	25.3
QY	313	RTANEKYLTAIYLDYMEELGMLL-GGRPTSTREOMQVYLEBIOLANTIVDOPORDEKTI	37.1
Db	254	KTENENEKVLGYLINVWVQGLKLGDDDEAIRQMOQILDPETALANTITPEKRRDEBLI	31.3
QY	372	YHKMSISEIOLAPSMIDMEFLSFLSPLESDSPRVVYVYGMVYLOQVSELIINTRESIL	43.1
Db	314	YHKVTAEBIQTOLAPALNMLPFLNTITFPYVEINSEPIVWYDKEXLEQISTLINTTDRCL	37.3
QY	432	NNVLIINVOKTSSILDRPFESAOEKLJETLYGTGKSCVPRMOTCISNTDADAFALGSL	49.2
Db	374	NNVMIINVLRKTISSFUDORFQADCEKMEVMTGKTCLPFWKCVSSTENULFALGPM	43.3
QY	492	FVAKTDFROSKEIAESGMTSEIRTAEEBALGOLVWMDKETROAKAEKADAIYMDIGPFDI	55.1
Db	434	FVAKTFAEDBSKSIATBILIEIKKAEBSISLTKMMDDETRKSAEKADAIYMIGYNFI	49.3
QY	552	LBEPKELDDVYDGEIYSEDSFFQNMMLNTYNFSKVMADOLKRPSPRDQMSMTPOTVNAYYL	61.1
Db	494	MDPEKELDKFNNYTVAPDLYFENANARFPNFSWRVYADOLKRAPRDQMSMTPRVNAVYYS	55.3
QY	612	PTKNEIYVPAGILLOAPYABANHPKXLANGGSIGVWVGHGLTHAIPDORREVDKESNLBPM	67.1
Db	554	PTKNEIYVPAGILLOAPFYTRSSPKXLANGGSIGVWVGHGLTHAIPDQGRREVDKQNLBPM	61.3
QY	672	QNESLAAPFNHTACMEBOYNOYQVWGEIRLANGROTLAGENIADNGKILKAAIYNAKAMLEKHG	73.1
Db	614	KNSSVAFIRKQRECHWEQYSNYSVNGEYVNNGHITLGENIADNGKILKAAIYRAYQVWVAKNG	67.3
QY	732	EBEOLPAVGLJNHOLFPPGFAOVWCSVTPPSSHGLVTPDHPSPARFRVLGTSLSNSDFL	79.1
Db	674	AHSLSPLTGLJNNLOLFLGFAOVWCSVTPPSSHGLITDHPSPSRFRVIGLSLSNSKFS	73.3
QY	792	RHRCPCVGSPPMNGOLCEVW 811	
Db	734	BHRCPCGSSPPMNPBKCEVW 753	

## RESULT 8

US-08-646-273-30  
Sequence 30, Application US/08646273  
Patent No. 606502  
GENERAL INFORMATION:  
APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,  
APPLICANT: Martin, Jacob, Elard, Oeter, Rainer, Subkowski, Thomas, Hilden, Heinz  
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Keil & Weinkauff  
STREET: 1101 Connecticut Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
COMPUTER: IBM AT-compatible, 80486 processor  
OPERATING SYSTEM: MS-DOS version 6.0  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,273  
FILING DATE: 16-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP94/03706  
FILING DATE: 11-NOV-1994  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 754 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-273-30

Query Match 60.0%; Score 2567.5; DB 3; Length 754;  
Best Local Similarity 59.6%; Pred. No. 1.2e-239;  
Matches 477; Conservative 119; Mismatches 154; Indels 51; Gaps 7;

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QY 14 MVEKATLDEDEPPEVPGASPDMEVG-KASPFSPGSGMTPGPRSSGLFMRV 72
DB 2 MSTYKRLTDEEDLVDSLSDDVYVNHQVFRG-----PRNGQRCW-- 43
QY 73 TCHLRISGLCSRTWGFQKGTROLGSRTOLEVLGASILLALLGLVALGYOYH 132
DB 44 -----AARTPVKRLVALLAALVALCLAVLGIGYQ 76
QY 133 -RDPSSHSTCTEACIRVAGKILSLDRGVSPCEDFYQSCGGWIRNPLPDGSRMNTFN 191
DB 77 TRFP--SVCLSEACISVTSSILSSMDPTVPCODFTYACGGMWKANVPDGHSRWGTFS 134
QY 192 SLMDONAILKHLLENTFNSSFAEQKQRFYLSCLQVERIEELAGPLRDLIKIGW 251
DB 135 NLMEHNOAIIKHLENT--ASVSEARKDDEYRACNRETRIEELKAKPLMELEKLGW 193
QY 252 NITSPMDQDNFMEVLLKAVAGTYRATPEFTVYISADSKSNSNVIOVDSGLFLPSRDYLL 311
DB 194 NITSPMDKDNFODTLQVTSYHSHYSPFSYVVSADSKSNSNVIOVDSGLGLPSRYYL 253
QY 312 NRTANEKYLTAVDYMEELGMLGGRPTST-REQMOVLELEIQLANTITVPQDRDEEK 370
DB 254 NKTENEKYLGLYLVNMQGLKGLCGADITRPMQOILDFETALANITTPQEKRRDEEL 313
QY 371 IYHMSISELOALASMDLEFLSLSPLELSEEVVYVGMVLOOVSELINRTEPSI 430
DB 314 IYHKVTAELQTLAPAINMLPELNTITYPVAINSEPIVYDKELSKVSTLNSTDKL 373
QY 431 LNNYLVNLYVQKTSILDRRPFESAQKLELTLYGKSCVPRMOTCISNTDLAGFALGS 490
DB 374 LNNYLVNLYVQKTSILDRRPFESAQKLELTLYGKSCVPRMOTCISNTDLAGFALGP 433
QY 491 LFPVATPDROSKEIAEGMISIRTAPEBALGQLVMDKTRQAAEKADAIYDMIGPDP 550
DB 434 MFPVATPDROSKEIAEGMISIRTAPEBALGQLVMDKTRQAAEKADAIYDMIGPDP 493
QY 551 ILPEKLELDVYDGEISBDSFQOMMLYNFSASVMDQARPSRPMOMTPTQVNAVY 610
DB 494 IMDEKLELDVYDGEISBDSFQOMMLYNFSASVMDQARPSRPMOMTPTQVNAVY 553
QY 611 LPTGNEIVFPAGILQAPFYARNHPRKALNFGIGVVMGHELTHAFDDGREYDEKGNLRPW 670
DB 554 SPTGNEIVFPAGILQAPFYARNHPRKALNFGIGVVMGHELTHAFDDGREYDEKGNLRPW 613
QY 671 WONESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGLKAAYNAVYAWLRKH 730
DB 614 WKNSSVBAFQKQIACMEYOYNGYVNGEPVNGRHTLGENIADNGLKAAYNAVYAWYKKN 673
QY 731 GEEQOLPAVGLTNHQLPFGVPAQVWCVTPRESSHEGLVYDHPSPARFVLTGTSNRDF 790
DB 674 GAEQTLPLGLTNHQLPFLSPAQVWCVTPRESSHEGLVYDHPSPARFVLTGTSNRDF 733
QY 791 LRHFQCPGVPMPNPGOLCEW 811
DB 734 SEHFHCPPGSPMNHKCEW 754

```

# RESULT 9

US-08-289-112-2  
Sequence 2, Application US/08289112  
Patent No. 5686640

GENERAL INFORMATION:  
APPLICANT: Yanagisawa, Masashi  
TITLE OF INVENTION: Endothelin Converting Enzyme-1: A  
TITLE OF INVENTION: Membrane-Bound Metalloprotease That Catalyzes The

TITLE OF INVENTION: Proteolytic Activation of Big Endothelin-1  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/289,112  
FILING DATE: 10-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:414/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-289-112-2

Query Match 59.5%; Score 2546; DB 1; Length 758;  
Best Local Similarity 59.8%; Pred. No. 1.4e-237; Indels 40; Gaps 7;

```

QY 23 RDEDAETP-VBEGASPDMEVGKASPPSPGMPGTGTRSSGLFMRVTCPLHRSIS 81
DB 4 RGQDLRSPLLSSEAP-----GLTSPFLRPLSPLOVNRGRNRCW----- 47
QY 82 GLCSRTWGFQKGTROLGSRTOLEVLGASILLALLGLVALGYOYH-RDPSSHSTC 140
DB 48 -----AARTPVKRLVALLAALVALCLAVLGIGYQRTF--SYC 87
QY 141 LPTACIRVAGKILSLDRGVSPCEDFYQSCGGWIRNPLPDGSRMNTFNSLMDONAI 200
DB 88 LSEGCTSVSSILSSMDPTVPCODFTYACGGMWKANVPDGHSRWGTFSNLMEHNOAI 147
QY 201 LKHLLENTFNSSFAEQKQRFYLSCLQVERIEELAGPLRDLIKIGMNTGPMPOD 260
DB 148 LKHLLENT--ASVSEARKDDEYRACNRETRIEELKAKPLMELEKLGWNTGPMPOD 206
QY 261 NFEVLLKAVAGTYRATPEFTVYISADSKSNSNVIOVDSGLFLPSRDYLLNRTANEKYL 320
DB 207 NFDPTLQVTSYHSHYSPFSYVVSADSKSNSNVIOVDSGLGLPSRDYLLNRTANEKYL 266
QY 321 TAYLVMEELGMLGGRPTST-REQMOVLELEIQLANTITVPQDRRDEEKIYHKISIE 379
DB 267 TGLANTVVOGLKGLGGAADITRPMQOILDFETALANITTPQEKRRDEELIYHKVTAEL 326
QY 380 LQALASMDLEFLSLSPLELSEEVVYVGMVLOOVSELINRTEPSILNNTYLVNLY 439
DB 327 LQTLAPAINMLPELNTITYPVAINSEPIVYDKELSKVSTLNSTDKLANNYLVNLY 386
QY 440 VQKTSILDRRPFESAQKLELTLYGKSCVPRMOTCISNTDLAGFALGSLFVKATFDR 499
DB 387 VRKTSFIDQRFPDADKEKMEVWYGTKTCIPLRMKFCVSDTEMTLGFALGPMVKATFAE 446
QY 500 QSKELIAGMISIRTAPEBALGQLVMDKTRQAAEKADAIYDMIGPDPFLPEKLELD 559
DB 447 DSKNIASEIILEIKKAFESLSTLKMDEDTKRSKAKADAIYNMIGYPIFMDPELDK 506

```

```

QY 560 YDDGEI SEDSFFQWMLNLYNFSAKYMAQOLRKPSPRDQWSTPCQVNAVYUPTKXIEYF 619
Db 567 VFNQDTAIPDLXFEHNAHMRFFNSKWTYADQOLKAKPRDQWSTPMPVMAVYSTTKXIEYF 566
QY 620 PAGIIQAPFYAANHHKALNFFGGIGVMMGHETLTHAFDDQGREYDKENGLRPMWONESLAAF 679
Db 567 PAGIIQAPFYTSRSPNALNFFGGIGVVGHETLTHAFDDQGREYDKDNLPRMWNKSIVEAF 626
QY 680 RNHTCMEEQYNOQVNGERLNGRQTLGKNIDNGKLKAAVNAKYLAKKHGEQOLPAV 739
Db 627 KQQAACMEQYGNVYNGEPVNGRHTLGENIDNGKLKAYRAYQYMWKNGABQTLPTL 686
QY 740 GLTNHQLFVFGPAQWVCSTRTPESSHGAVTDPHSPARFVIGTLTSSRDLPLRHPCGPYV 799
Db 687 GLTNHQLFPLSGQWVCSTRTPESSHGELITDPHSPRFRVIGTISNSKRFSEHFHCPPG 746
QY 800 SPMPGOLCEW 811
Db 747 SPMPHKECW 758

RESULT 10
US-08-646-273-23
; Sequence 23, Application US/08646273
; Patent No. 6066502
GENERAL INFORMATION:
APPLICANT: Kroeger, Burkhard, Seulnerger, Harald, Meyer, Thomas, Schmidt,
APPLICANT: Martin, Jacob, Elard, Oetler, Rainer, Sudkowski, Thomas, Hille, Heinz
TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauff
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,273
FILING DATE: 16-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03706
FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-273-23

Query Match 59.3%; Score 2539.5; DB 3; length 708;
Best Local Similarity 64.8%; Pred. No. 5,4e-237;
Matches 461; Conservative 110; Mismatches 135; Indels 5; Gaps 4;

QY 103 TQLELVLAGASILLALALILGLCLVALGVQYH-RDPSSHSTCLTEACTRVAGKTIIESLDRGVS 161
Db 1 TPVEGRVLVVALLAALVALVCLAVLGIQYQRTTP--SVCLSRACISVTSIILSMDPTVD 58
QY 162 PCEDFYQFSCGGMIRRNPLPDGRSRWNTFNSLMDONQALILKHLLENTTNNSSSEABQKTQ 221
Db 59 PCDFEFTYACGGMIRANVPDPDHSRWGTFNSLMENHQAIIKILLENST-ASVSEABERKQ 117
QY 222 RFLVSLQVERIEELGAQPLRIELKIGGMNITGPDQONFHEVLKAVAGTYRATPFYV 281
Db 118 EYTRACNMEIIEELKAKPLMEILKGLGGMNITGPDKNFQDTLQVVTSHYHTSPFSV 177

```

QY 282 IISADSKSSNNVAVQDQSGFLPSPRDYYLNRITAEKYLTAIVADYMEELGMLLGRPTST 341  
 178 IYASADSKSSNNVAVQDQSGFLPSPRDYYLNRITAEKYLTAIVADYMEELGMLLGRPTST 237  
 QY 342 -REOMQVLELEIOLANITVPDQORRDEKILYHKMSISELQALAPSMDLLEFLSLSBL 400  
 238 IRPQMOQLDEPETAALANITTIPOEKRRDEBELYHKVTALEQLTADAINMLPLINTTIFYEV 297  
 QY 401 ELASSEPVRVYGMVYLOQVSELINRTEPSILANNYILNNLVQKTTSSLDPRFESSAQKLEL 460  
 298 EINESSEPIVYDKYLSKYSTLINSTDKCLANNVMIWMLVKTSSPFLQRFQDADEKEME 357  
 QY 461 TLVYKKSQVVRMOTCISINTDQALGFALGSLFVKATPDRQSSKEIABGMSIERTAFEEAL 520  
 358 VMGTGKTCCLPRMFCVSDTENTLGFALGPMFVKATPDRQSSKEIABGMSIERTAFEEAL 417  
 QY 418 STLMKMBEDTRKSAKEKADALYNNIGVNFIMDPRELKQVFNDYVAVPDLVYENAMRFPN 477  
 QY 581 FSAVYAADQLRKPSPSDQWMTPTQVNAYYILPTKNEIYFPACILQAPFYARHPALANG 640  
 478 FSWRVTDQLRKAQNRQDQWMTPTQVNAYYISPTKNEIYFPACILQAPFYARHPALANG 537  
 QY 641 GIGVYVGHETLHAQPDQREYDKEGNLRPMQONESLAFRHHTAQMBEYOANYOUNGERL 700  
 538 GIGVYVGHETLHAQPDQREYDKEGNLRPMQONESLAFRHHTAQMBEYOANYOUNGERL 597  
 QY 598 NGRHTLGENIADNGGLKAYRAYQYQWVKKNGAEQTLPTLGLTNNOLFLFSFAQWCVSXT 657  
 QY 761 PESHEGLVNDPHSPARPRVYGTLSNSRDLRHCPCPGSPNNPQQLCEW 811  
 658 PESHEGLVNDPHSPARPRVYGTLSNSRDLRHCPCPGSPNNPQQLCEW 708  
 Db  
 RESULT 11  
 US-08-646-273-25  
 Sequence 25, Application US/08646273  
 Patent No. 6066502  
 GENERAL INFORMATION:  
 APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,  
 Applicant: Martin, Jacob, Elard, Ofter, Rainer, Subkowski, Thomas, Hillen, Helinz  
 TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Keil & Weinkauff  
 STREET: 1101 Connecticut Avenue  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage  
 COMPUTER: IBM AT-compatible, 80486 processor  
 OPERATING SYSTEM: MS-DOS version 6.0  
 SOFTWARE: Wordperfect version 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/646,273  
 FILING DATE: 16-NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP94/03706  
 FILING DATE: 11-NOV-1994  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 703 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-646-273-25

59.2%; Score 2534.5; DB 3; Length 703;  
CE 4%; Prod 150335.

Query Match	59.2%;	Score 2534.5;	DB 3;	Length 703;
Best Local Similarity	65.4%;	Pred. No. 1.6e-236;		
Matches 458;	Conservative 113;	Mismatches 124;	Indels 5;	Gaps 4;

QY	114	LLAALLGCUVALVOYH-RDPSHSTCTEACIRPAGLIEBIDGVSRCBEFYOSGC	172
Db	7	VLLAAGLVAACALALGQYOTRSP--SVCLSEACVASTSSILSDHFTVPCDHFFSACG	64
QY	173	GWIRBNPLPDGRSRWNTFNSLWDONQALIKHLENTFNSSSBAEOKTORFYILSCQVER	232
Db	65	GWIKANPYVDGHSRWGTFNSTLWEHNOALIKHLENTST-ASVSAEKRAQYVYRACNNETR	123
QY	223	IEELGAOPLRDLIEKIGGNITGPMWQDPMFELKAVAGTYRATPPEFYIASDSKSSNS	292
Db	124	IEELAKPLMELIERGGWNTITGPMAKNDPQDTLOVYTAHYRTSPFSYVVSADSNSSNS	183
QY	293	NVIQVDSGLFPLSRDYINRTANKEVLYLAAYLDYMEELGML-GGRPTSTREMOQVLET	351
Db	184	NVIQVDSGLFPLSRDYINRTANKEVLYLAAYLDYMEELGML-GGRPTSTREMOQVLET	243
QY	352	EIQLANITYPOQDRDEEKIYHKMSISELOALAPSDMLFELSLPLSELSDEPVVY	411
Db	244	ETALANITIPQEKRRDEELIYHKVTAEBQTLAPALNMLPFLNTIYVPAINESEPIVY	303
QY	412	GMDYVQOYSELNTRPEPSILNNYLLWNLYOKTSSLDRRPESAOEKLLETLYTKSCVP	471
Db	304	DKEYLEQJSTLINTTDRCLANNYIMVLRKISSFLDQRFQDADKRFMEVMTIKTKICLP	363
QY	472	RMQTCISNTDIALGPAIGSLFYVKATFDRQSKETABGMSIERTAPAEALGQLVMDKTR	531
Db	364	RWKFVCVSTENNIGFALGMPFYKATFAEDSKSIATITILIEIKKAPFESISLTLMDBETR	423
QY	532	QAASEKADAIYMGIPPDPILEPEKELDYVDGIEISEDFQOMLWLYNFSAKVAMDOR	591
Db	424	KSAREKADAIYMGIPPDPILEPEKELDYVDGIEISEDFQOMLWLYNFSAKVAMDOR	483
QY	592	KPESDQWSMTBOTVNAVYLLPTKNEIVFPAGILQAPFYARNHPKALNFGIGVYMGEILT	651
Db	484	KAPNDDQWSMTBOTVNAVYLLPTKNEIVFPAGILQAPFYARNHPKALNFGIGVYMGEILT	543
QY	652	HAFFDQGREYDEGNLRPMWONESLAAFNNHTACOMEQONOVYONNEBRLNGRQTLGENTA	711
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QY	712	DNGGLKAAYNAYKAWLRKHGEBQOLPAVGLJNHQLEFFVGAQYCVSRTPRESSHEGLYTD	771
Db	604	DNGGLKAAYNAYKAWLRKHGEBQOLPAVGLJNHQLEFFVGAQYCVSRTPRESSHEGLYTD	663
QY	772	PHSPARFVLTGLTNSRDLRHFPGCVGSPMNPQGLCEVW	811
Db	664	PHSPARFVLTGLTNSRDLRHFPGCVGSPMNPQGLCEVW	703

RESULT 12  
 US-08-646-273-19  
 : Sequence 19, Application US/08646273  
 : Patent No. 6066502  
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 : GENERAL INFORMATION:  
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 : APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,  
 : Applicant: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hille, Heinz  
 : TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).  
 :  
 : NUMBER OF SEQUENCES: 36  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Keil & Weinkauf  
 : STREET: 1101 Connecticut Avenue  
 : CITY: Washington  
 : STATE: D.C.  
 : COUNTRY: USA  
 :  
 : ZIP: 20036  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

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COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,273
FILING DATE: 16-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03706
FILING DATE: 11-NOV-1994
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-273-19

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Query Match	47.84;	Score 2047;	DB 3;	Length 567;
Best Local Similarity	65.54;	Pred. No. 2,3e-189;		
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				Gaps 2;

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Qy	243	DLJEKIGMNIITGPMDDNFMENVLKAVAGTYRATPEFFTVYISADSKSNSNVIOVDSGL	302
Dd	60	ELIEKCGMNIITGPMDKDNFQDTLOVVTSHYHTSPFSSVYVADS KNSNSNVIOVDSGL	119
Qy	303	FLPSRDYYLNKRTANEKULTAYLDYMEELGMLGGRPIST-REOMQVYLELEIQLANTIVP	361
Dd	120	GLPSRDYYLNKTEKEKULTYLYNMWOLGKLGGGABDITRPMQOITLDEFTALANTITIP	179
Qy	362	QDORDEEKTYHKXISELOALAPSMDELFLSFLSPLSESPVNVVYGMDLOQVSE	421
Dd	180	QEKRDEBELYHKYTAELQTLAPAINWLFPLWITPYPVEINSESEPIVIDKEKELSKVST	239
Qy	422	LINTEBSILNNYLINWLVOKTSSLDLRFPESAOKLELTLYGTKSCVPRMOTCISNTD	481
Dd	240	LINSTDKCLNNWMIYMLVKRTSSFLDQRFQDADKEKMEVNYGTKYKCLPRMKCVADTE	299
Qy	482	DALGFALGSLFVYATFPROSKETAEGBISIRTAFEALQOLVMMDEKTOAKKEXDAI	541
Dd	300	NTLGFALGPMFVATFAEDSKNIASELITLIIKKAFEESLSTLKMWDTEKSAEKXDAI	359
Qy	542	YDMIGPEDFLEPEKELDDVDDYEISEDSFQNNLNIYNNSAKYMAQOLKRPSPRDQSM	601
Dd	360	YNMIGYFNFIIDPREDLKVFRNDITYAVDLYFENAMRFPNFSWKVATDQLKAPRRDQSM	419
Qy	602	TPQTVNAVYULPYTKNEIVFPAGILQAPFYABNHPRKALNFGSIGVVMGHELTFAFDQGREY	661
Dd	420	TPPVNAVYUSPTKNEIVFPAGILQAPFYTRSSPVALNFGSIGVVMGHELTFAFDQGREY	479
Qy	662	DKGANLPRWQONSLAFLRHHRTACMEQCNQOYQVNGERLNGRQTLGENIADNGILKAYN	721
Dd	480	DKGANLPRWKNSSVEFAFKOOTACMWOYGNTSVNGEVPVNGRHTLGENIADNGILKAYR	539
Qy	722	AYKAMLRKHGBEQLPAVGLTNHQLFEV	749
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RESULT 13
US-09-704-611-2
; Sequence 2, Application US/09704611
; Patent No. 6548284
; GENERAL INFORMATION:
; APPLICANT: JCR Pharmaceuticals Co., Ltd.
; TITLE OF INVENTION: Membrane-bound Metalloprotease and Soluble Secreted F
; FILE REFERENCE: GP30
; CURRENT APPLICATION NUMBER: US/09/704,611
; CURRENT FILING DATE: 2000-11-03

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Search completed: July 3, 2004, 20:09:28  
Job time : 24 secs

GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham Plc  
TITLE OF INVENTION: No. 6255468el Compounds  
FILE REFERENCE: GP30124  
CURRENT APPLICATION NUMBER: US/09/305,640B  
CURRENT FILING DATE: 1999-05-05  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 775  
TYPE: PRT  
ORGANISM: Homo sapiens  
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Best Local Similarity 36.6%; Pred. No. 4.9e-126; Mismatches 272; Indels 90; Gaps 19;

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QY 257 ----WDQDNFMEVLKAVAGTYRATPFTTYISADSKSSNSNVTQVDQSLFLPSRDYYLN 312  
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AUTHORS  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carminci, P.,  
Komori, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
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RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

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20530913  
11076861

TITLE  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

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AUTHORS  
5  
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Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

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6  
(bases 1 to 2496)  
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kashiwagi, K.,  
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Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N.,  
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.  
Location/Qualifiers

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1157 GCTGAGTTGAGATCAAGCTGAGCAATCAAGTGCCTCAGAGCAAGAGGCGCGAGCA 1216  
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Db 1066 GCTGAGCTGAGATACAGCTGGCTAACATCACTGTGCCCCAGGACCAAGGCGGTATGA 1125  
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AK043473  
VERSION  
AK043473.1 GI:26089750  
ACCESSION  
HTC; CAP TRAPPER.  
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ORGANISM  
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REFERENCE  
AUTHORS  
TITLE  
Garinici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL  
MEDLINE  
PUBMED  
20499374  
11042159

REFERENCE  
AUTHORS  
TITLE  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, N., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL  
MEDLINE  
PUBMED  
20530913  
11076861

REFERENCE  
AUTHORS  
TITLE  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6  
(bases 1 to 1850)  
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imetani, K., Ishii, Y., Itoh, M., Kagawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,





**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgabgs-r@mail.nih.gov](mailto:cgabgs-r@mail.nih.gov)  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LLAM2722 row: 9 column: 13  
 High quality sequence stop: 650.

**FEATURES**

source

1. .1156

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAG:5727780"

/issue\_type="hippocampus"

/lab\_host="DH10B"

/clone\_1ib="NIH MGC 124"

/note="Organ: brain; Vector: PCMV-SpOre; Site 1: EcorV (destroyed); Site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

**ORIGIN**

Query Match 21.2%; Score 714.6; DB 12; Length 1156;  
 Best Local Similarity 94.1%; Pred. No. 5.8e-93;  
 Matches 766; Conservative 0; Mismatches 44; Indels 5; Gaps 4;

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 1689 ATGATGAGAAGACCGCCGACGACGACGACGACGACGATGCCATCTATGATGAT 1748  
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 1869 ATGCTGACAGCTCGGCAAGCTCTCCAGCGGACGACGACGACGACGACGACGACG 1928  
 241 ATGCTGACAGCTCGGCAAGCTCTCCAGCGGACGACGACGACGACGACGACGACG 300  
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 481 AACCTGCGGCGCTGTGCGGCAAGTCTTGGCAGCCTTCCGGAACCAACGAGCTTCG 540

QY 2169 ATGAGGAACAGTACATATACAGAGTCAATGGGAGAGGCTCAACGCGCGCAGAGC 2228  
 DB 541 ATGAGGAACAGTACATATACAGAGTCAATGGGAGAGGCTCAACGCGCGCAGAGC 600  
 QY 2229 CTGGGGAGAACATTGCTGACACAGCGGGGCTGAAGGCTGCTACATGCTTACAAAGCA 2288  
 DB 601 CTGGGGAGAACATTGCTGACACAGCGGGGCTGAAGGCTGCTACATGCTTACAAAGCA 660  
 QY 2289 TGGCTGAGAAAGCAT-GGGAGAGAGACGACATCTGCCAGCGGTGGG-CTCACCAACACC 2346  
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 QY 2347 AGC-TCCTGTTGGGATTTGGCC-AGGTGAGTCTGGATCGGACACGACGAGAGCT 2403  
 DB 721 AGCTTCTTCTCTGAGATTTGGCCAGGTGAGGAGCTGGGACCGACGACCGGAAAGC 780  
 QY 2404 CTCACGAGGGGCTGTGACCGACCCCAACGCGCTGCGCTTCCGCGTGTGGG 2458  
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**RESULT 4**

BU739636/c 712 bp mRNA linear EST 10-OCT-2002  
 LOCUS UI-E-EJ0-aho-n-24-0-UI-81 UI-E-EJ0 Homo sapiens cDNA clone  
 DEFINITION UI-E-EJ0-aho-n-24-0-UI 3', mRNA sequence.  
 ACCESSION BU739636  
 VERSION BU739636 GI:23678186  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
**AUTHORS** (bases 1 to 712)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
**TITLE** Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PubMed 8889548

**COMMENT**

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: [bento-soares@iowa.edu](mailto:bento-soares@iowa.edu)  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics ([www.resgen.com](http://www.resgen.com)).  
 Seq primer: MJ3 FORWARD  
 PolA=Yes.

**FEATURES**

source

1. .712

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-EJ0-aho-n-24-0-UI"

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 optic nerve, retina, Retina foveal and Macular, RPS and  
 Choroid"

/dev\_stage="fetal and adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_1ib="UI-E-EJ0"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Ecor I; Site 2: Not I;  
 UI-E-EJ0 is a subtracted cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double



stranded cDNA was ligated to an EcoR I adaptor, digested with Notc I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Notc I site and the (dT)<sub>18</sub> tail. The sequence tags for this library are: fetal eyes, AGAATCAAG; lens, CGATTAGCGA; eye anterior segment, AATCCCGCAT; optic nerve, CCATTAGTGT; retina, CCGCGT; Retinal Foveal and Macular, GTCC; RPE and Choroid, AGCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NIH).  
TAG\_LIB=UI-B-EJ0  
TAG\_TISSUE=foveal and Macular Retina  
TAG\_SEQ=GTCC"

Db	246	GATCTGAAACCTGGTGAAGAAAGCAACCTCAAGCTTGACCGAGCTTTGAGTGTGCACA	305
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Qy	1538	CTGCATCTCCAAACAGGATGACGCCCTTGGGCTTTGGGAGTCCCTCTTGATGAAGGC	1597
Db	366	CTGCATCTCCAAACAGGATGACGCCCTTGGGCTTTGGGAGTCCCTCTTGATGAAGGC	425
Qy	1598	CACGTTTGACCGGCAAAAGAAATTTGACAGAGGATGATCAAGCAATCCGACCGC	1657
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Qy	1658	ATTGAGAGAGGCGCTGGGACAGCTGCTTTGGATGATGAGAAGACCGGCCAGAGCCAA	1717
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Qy	1718	GGAGAAACCAATGCAATCATTAATGATATGTTTCCCAACCTTAATCCGAGAGCCCA	1777
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Qy	1778	AGAGCTGATGATGTTTATGACAGGATGCAAAATTTCTGAAGATTTCTTCCAAACAT	1837
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Qy	1838	GTTGAATTTGTACAACCTTCTCT	1859
Db	665	GTTGAATTTGTACAACCTTCTCT	686
RESULT 6			
AV708732			
LOCUS	AV708732	691 bp	mRNA linear EST 09-OCT-2000
DEFINITION	AV708732	ADC Homo sapiens cDNA clone ADCAXE12 5', mRNA sequence.	
ACCESSION	AV708732		
VERSION	AV708732.1	GI:10725997	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 691)		
AUTHORS	Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J., and Han,Z.		
TITLE	Homo sapiens cDNA ADC clones		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex. 45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.		
FEATURES			
source	location/Qualifiers		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="ADCAXE12"		
	/tissue_type="Adrenal gland"		
	/dev_stage="Adult"		
	/lab_host="SOLR"		
	/clone_id="ADC"		
	/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"		
ORIGIN			
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Best Local Similarity	98.1%;	Pred. No. 1.2e-83;	

	Matches	678;	Conservative	0;	Mismatches	11;	Indels	2;	Gaps	2;		
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QY	2408	CGAGGGG	GTGTGA	CCGAC	CCCCCA	CAGCCCTG	CCGCTTCG	CCGTGTG	GGGCA	CTCTCTC		2467
Db	121	CGAGGGG	GTGTGA	CCGAC	CCCCCA	CAGCCCTG	CCGCTTCG	CCGTGTG	GGGCA	CTCTCTC		180
QY	2468	CAACTCC	CGTGACTT	CCCTG	CGGGCA	CTTCCG	CTGCTGTGTG	GGGCTCCCC	CATGA	ACCAAG		2527
Db	181	CAACTCC	CGTGACTT	CCCTG	CGGGCA	CTTCCG	CTGCTGTGTG	GGGCTCCCC	CATGA	ACCAAG		240
QY	2528	GCACCTGT	GTGAGGTGTG	TGATGA	CACTGGAT	TCAGGGG	AGAAA	TGCGCC	AGCTGTCA	CCAGAC		2587
Db	241	GCACCTGT	GTGAGGTGTG	TGATGA	CACTGGAT	TCAGGGG	AGAAA	TGCGCC	AGCTGTCA	CCAGAC		300
QY	2588	CTGGGGG	CAGCTCT	CTCTGA	CAAAAG	CTGTTG	CTTGGGG	TTGGAGA	AGCAAT	ATGCAAG		2647
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QY	2648	TGGGCTGG	GTCTAGT	TCCCTC	CCCCCA	CAGGTGA	CATGAGTA	CAGACC	TTCTCT	CAATCAC		2707
Db	361	TGGGCTGG	GTCTAGT	TCCCTC	CCCCCA	CAGGTGA	CATGAGTA	CAGACC	TTCTCT	CAATCAC		420
QY	2708	CACATTG	TGCTCT	TGCTTTT	GGGGGG	TGCCCT	CTGCTCC	AGCAGAG	CCCCCA	CATTCACTG		2767
Db	421	CACATTG	TGCTCT	TGCTTTT	GGGGGG	TGCCCT	CTGCTCC	AGCAGAG	CCCCCA	CATTCACTG		480
QY	2768	TGACATCT	TTCCG	TGTCA	CCCTGTG	CTGGA	AGAGGTCT	GGGGT	GGAGG	CCAGTTCC	CATA	2827
Db	481	TGACATCT	TTCCG	TGTCA	CCCTGTG	CTGGA	AGAGGTCT	GGGGT	GGAGG	CCAGTTCC	CATA	540
QY	2828	GGAAGAG	ATGCTG	CTCTT	CTGTCC	CCAGAG	GTCACT	CAGCTTG	GGCGGC	CACTGGGCC		2887
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QY	2948	CTTCACTA	GTGCGCA	CTTTAG	GGGGTGA	CTCA						2978
Db	659	CTTCACTA	GTGCGCA	CTTTAG	GGGGTGA	CTCA						699

	RESULT 7	
CBSI19973		
LOCUS		
DEFINITION	CBSI19973	732 bp mRNA linear EST 09-JUL-2003
ACCESSION	UI-M-iid-cek-o-21-0-ui.r1 NIH-BMAP G10 Mus musculus cDNA clone IMAGE:6840910 5' , mRNA sequence.	
VERSION	CBSI19973	
KEYWORDS	CBSI19973..1 GI:29353328	
SOURCE	EST.	
ORGANISM	Mus musculus (house mouse)	
TAXID	Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1 (bases 1 to 732)		
NIH-WGC http://mgc.nci.nih.gov/.		
National Institutes of Health, Mammalian Gene Collection (MGC)		
Unpublished (1999)		
Contact: Robert Strausberg, Ph.D.		
Email: cgabbe@remail.nih.gov		
Tissue Procurement: Dr. Jim Lin, University of Iowa		
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		



```

Db      1 GGAAGAGATCTACACAGATGAGCATTTCGGAGCTGCAAGCTCTGCGCCCTCCATGGA 60
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Db      61 CTGGCTTGAAGTCTCTGCTCTTCTTCTGCTGTCACCAATTGAGTGAAGTCTGAGCTGT 120
QY      1337 GGTGTGTATGGATGATTAATTTCGAGAGGTGTCAGACTCATCAACCGCAGAAC 1396
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QY      1397 AACCATCTGCAACAATTACCTGATCTGGAACCTGTGCAAAAGACAACCTCAAGCTGGA 1456
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Db      601 AGATCTTTCTTCCAAACATG 622

RESULT 9
LOCUS   BM713622          596 bp      mRNA      linear      EST 28-FEB-2002
DEFINITION
UI-B-EJ0-aho-n-24-0-UI.r1 UI-B-EJ0 Homo sapiens cDNA clone
VERSION  BM713622
KEYWORDS
SOURCE   EST.
ORGANISM Homo sapiens (human)
          Homo sapiens
          Bukayvora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 596)
          Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
JOURNAL  MEDLINE
PUBMED   97044477
          8889548
COMMENT  Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          Tissue Procurement: Dr. Gregg Hageman
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

```

```

FEATURES
source
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Researchers may obtain clones from Research
    Genetics (www.reagen.com).
    Seq primer: M13 Reverse.
    Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="UI-B-EJ0-aho-n-24-0-UI"
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            Choroid"
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            /lab_host="PH10B (life Technologies) (T1 phage resistant)"
            /clone_1lb="UI-B-EJ0"
            /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
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            UI-B-EJ0 is a subtracted cDNA library constructed
            according to Bonaldo, Lennon and Soares, Genome Research,
            6:791-806, 1996. First strand cDNA synthesis was primed
            with an oligo-dT primer containing a Not I site. Double
            stranded cDNA was ligated to an EcoR I adaptor, digested
            with Not I, and cloned directionally into pT73-Pac
            vector. The oligonucleotide used to prime the synthesis of
            first-strand cDNA contains a library tag sequence that is
            located between the Not I site and the (dT)18 tail. The
            sequence tags for this library are: fetal eyes,
            AGATTCAGAG; lens, CGATTAGAG; eye anterior segment,
            AATGCCGAT; optic nerve, CCATTAGAG; retina, CCGCG; Retina
            Foveal and Macular, GTCG; RPE and Choroid, ACTTA. This
            library was created for the program Gene Discovery in the
            Visual System, supported by National Eye Institute (NEI)."

Query Match      17.5%; Score 592.4; DB 12; Length 596;
Best Local Similarity 99.5%; Pred. No. 2.2e-75;
Matches 593; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ORIGIN
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Db      2375 GTGGTCTGTGGTCCGACACACAGAGCTCTACAGAGGGGCTGTGACCCGACAG 2434
QY      61 GTGGTCTGTGGTCCGACACACAGAGCTCTACAGAGGGGCTGTGACCCGACAG 120
Db      2435 CCCTGCGCGCTTCCGGGTCTGGGCACTCTTCAACTCCCGGACTTCTCTGGGCACTT 2494
QY      121 CCCTGCGCGCTTCCGGGTCTGGGCACTCTTCAACTCCCGGACTTCTCTGGGCACTT 180
Db      2495 CCGCTGCGCTTCCGGGTCTGGGCACTCTTCAACTCCCGGACTTCTCTGGGCACTT 2554
QY      181 CCGCTGCGCTTCCGGGTCTGGGCACTCTTCAACTCCCGGACTTCTCTGGGCACTT 240
Db      2555 GATCAGGGGAGAAATGCCAGCTGTACACAGACCTTGGGCACTCTCTGACAAAGCTGT 2614
QY      241 GATCAGGGGAGAAATGCCAGCTGTACACAGACCTTGGGCACTCTCTGACAAAGCTGT 300
Db      2615 TTGCTCTTGGGTTGGAGAGAAATGCAAGCTGGGCTGTGCTGCTCTCCGCCCA 2674
QY      301 TTGCTCTTGGGTTGGAGAGAAATGCAAGCTGGGCTGTGCTGCTCTCCGCCCA 360
Db      2675 CAGGTGACATGAGTACAGACCTCTCTGAATCAACCATTTGCTGCTTTGGGGGTGC 2734
QY      361 CAGGTGACATGAGTACAGACCTCTCTGAATCAACCATTTGCTGCTTTGGGGGTGC 420
Db      2735 CCTGCTCCAGACAGACCCCAACATTCATGATCACTTCCGTGCAACCTGCGCTG 2794
QY      421 CCTGCTCCAGACAGACCCCAACATTCATGATCACTTCCGTGCAACCTGCGCTG 480
Db      2795 GAAGAGTCTGGGTGGGAGGCGCAATTCATAGAGAGGCTGCTCTGTCGCCA 2854
QY

```

Db 481 GAAGAGGTCTGGGTGGGAGGCGCAGTTCACATAGGAAGAGTGTGCTTTGTGTCNCCA 540

QY 2855 GGCTCACTCAAGCTTGGGGCCATGGGGCCCTGCGCTGCTTCCCACTGTATCCAC 2910

Db 541 GGCTCACTCAAGCTTGGGGCCATGGGGCCCTGCGCTGCTTCCCACTGTATCCAC 596

RESULT 10

CB519920 704 bp mRNA linear EST 09-JUL-2003

LOCUS U1-M-G10-cek-e-23-0-UT.r1 NIH\_BMAP\_G10 Mus musculus cDNA clone

DEFINITION IMAGE:6840672 5', mRNA sequence.

ACCESSION CB519920

VERSION CB519920.1 GI:29353275

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS NIH-MGC

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

NIH-MGC Procurement: Dr. Jim Lin, University of Iowa

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES

source

Location/Qualifiers

1..704

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6840672"

/rname\_type="whole brain"

/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_1lb="NIH\_BMAP\_G10"

/note="Organ: Brain; Vector: PYX-Anc; Site 1: Exon I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Anc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chin, Ph.D., program coordinator."

ORIGIN

Query Match 17.1%; Score 578.8; DB 14; Length 704;

Best Local Similarity 86.8%; Pred. No. 1.9e-73;

Matches 625; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1396 CAAGACTCTGAACAATTACCTGATCTGGAACCTGTGCAAAAGACAACCTCAAGCTGG 1455

Db 1 CAGGCAATCTGAACAATTACCTAATTGGAACCTGTGACAGACACACCTCAAGCTTG 60

QY 1456 ACCGAGCCTTGAAGTCTGACACAGAGAGCTGTGAGAGCCCTTATGGAAGT 1515

Db 61 ACCAGCCTTGAAGTCTGACACAGAGAGAGCTGTGAGAGCCCTTATGGAAGT 120

QY 1516 CCTGTGTGCGGAGGTGGAGACCTGATCTCAACAGGATGAGCCCTTGGCTTTGCTT 1575

Db 121 CTTGACTCTGAGGTGGAGACCTGATCTCAATACAGATATAGCTTGGCTTTGCTC 180

QY 1576 TGGGGTCCCTCTTGTGAAGGCCACGTTTACCGGCAAGCAAAATTTGACAGGGGA 1635

Db 181 TGGGTTCACTTTTGGAAAGCCACATTTGACCAAGCAAGAAATTCGCCAGGGGA 240

QY 1636 TGATCAGCAAAATCCGAGACCGCATTTGAGAGAGCCCTGGGACAGCTGTTTGGATGAT 1695

Db 241 TGATCAATAAATCCGCTCTGCTTTTGAAGACACCTGGAGACCTTGTGATGATGATG 300

QY 1696 AGAAGACCCGCGAGGACGAGCAAGAGAAAGACATGSCATCTATGATATGATGTTTCC 1755

Db 301 AGAAGACCCGCGAGGACGAGCAAGAGAAAGACATGSCATCTATGATATGATGTTTCC 360

QY 1756 CAGACTTTATCTGTGAGCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATG 1815

Db 361 CTGATTTATCTGTGAGCCCAAGAGCTGATGATGATGATGATGATGATGATGATGATG 420

QY 1816 AAGATTCTTTCTTCCAAACATGTTGAATTTGTACACTTCTTCCCAAGTTATGCTG 1875

Db 421 AAGATTCTTTCTTCCAAACATGTTGAATTTGTACACTTCTTCCCAAGTTATGCTG 480

QY 1876 ACCAGCTCGCAAGCCTCCGAGCCGAGACAGTGGAGCATGCCCCAGACATGATG 1935

Db 481 ACCAGCTCGCAAGCCTCCGAGCCGAGACAGTGGAGCATGCCCCAGACATGATG 540

QY 1936 CCTACTACCTTCCAACTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1995

Db 541 CTACTACCTTCCAACTAAGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 1996 TCTATGCCCGCAACACCCCAAGCCCTGAATTCGTGGGCAATCGGTGGTCAATGGGCG 2055

Db 601 TCTATGCCCGCAACACCCCAAGCCCTGAATTCGTGGGCAATCGGTGGTCAATGGGCG 660

QY 2056 ATGAGTTGACGATGCTTGTGATGACCAAGGCGGAGATGATGATGATGATGATGATG 2099

Db 661 ATGAGTTGACGATGCTTGTGATGACCAAGGCGGAGATGATGATGATGATGATGATG 704

RESULT 11

AU296410 651 bp mRNA linear EST 17-JUL-2003

LOCUS AU296410 full-length enriched pig cDNA library, main and accessory

DEFINITION Olfactory bulb Sus scrofa cDNA clone olf\_101\_A12 5', mRNA sequence.

ACCESSION AU296410

VERSION AU296410.1 GI:32948973

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 651)

AUTHORS Fujisaki, S., Hiraiwa, H., Eguchi, T., Watanabe, Y., Honma, D.,

TITLE Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

JOURNAL Construction of a full-length library of swine olfactory bulb and

COMMENT its preliminary characterization

Unpublished (2003)

Contact: Seiichi Fujisaki

National Institute of Agrobiological Sciences

2 Ikenodai, Kunitzaki, Inashiki, Ibaraki 305-0901, Japan

Tel: 81-298-38-8659

Fax: 81-298-38-8659

Email: [seifuji@affrc.go.jp](mailto:seifuji@affrc.go.jp).

FEATURES

source

1..651

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone="OLF\_101\_A12"













GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 20:05:51 ; Search time 26 Seconds  
(without alignments)  
3000.436 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSPPMNPQLCEWV 811

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3662	85.5	825	2	endothelin convert
2	2592.5	60.6	770	2	endothelin convert
3	2586.5	60.4	754	2	endothelin convert
4	2567.5	60.0	754	2	endothelin convert
5	2561	59.8	758	2	endothelin convert
6	2546	59.5	758	2	endothelin convert
7	1440	33.6	774	2	endothelin convert
8	1282.5	30.0	750	1	neprilysin (EC 3.4
9	1272.5	29.7	750	1	neprilysin (EC 3.4
10	1199.5	28.0	751	1	neprilysin (EC 3.4
11	1192.5	27.9	750	2	neprilysin (EC 3.4
12	1192.5	27.9	750	2	neprilysin (EC 3.4
13	1122.5	26.2	590	2	neprilysin (EC 3.4
14	994.5	23.2	769	2	neprilysin (EC 3.4
15	958.5	22.4	732	1	neprilysin (EC 3.4
16	937	21.9	754	2	neprilysin (EC 3.4
17	892	20.8	700	2	neprilysin (EC 3.4
18	878.5	20.5	706	2	neprilysin (EC 3.4
19	760	17.8	667	2	neprilysin (EC 3.4
20	758.5	17.7	663	2	neprilysin (EC 3.4
21	747	17.4	1889	2	neprilysin (EC 3.4
22	673.5	15.7	823	2	neprilysin (EC 3.4
23	614	14.3	798	2	neprilysin (EC 3.4
24	590.5	13.8	801	2	neprilysin (EC 3.4
25	562.5	13.1	630	2	neprilysin (EC 3.4
26	561.5	13.1	630	2	neprilysin (EC 3.4
27	550	12.8	627	2	neprilysin (EC 3.4
28	549	12.8	627	2	neprilysin (EC 3.4
29	545	12.7	627	2	neprilysin (EC 3.4

30	513	12.0	564	2	probable zinc meta
31	510	11.9	726	2	protein F18A12.1
32	506.5	11.8	774	2	hypothetical prote
33	457.5	10.7	649	2	protein F18A12.6
34	375	8.8	732	2	hypothetical prote
35	366.5	8.6	651	2	hypothetical prote
36	349	8.2	658	2	hypothetical prote
37	341	8.0	534	2	hypothetical prote
38	330.5	7.7	570	2	protein F18A12.3
39	315	7.4	684	2	hypothetical prote
40	294	6.9	734	2	protein F18A12.4
41	225.5	5.3	817	2	hypothetical prote
42	176.5	4.1	550	2	protein F18A12.5
43	172.5	4.0	198	2	protein T06D4.5
44	172.5	4.0	198	2	hypothetical prote
45	148.5	3.5	491	2	hypothetical prote

## ALIGNMENTS

## RESULT 1

146078  
endothelin converting enzyme (EC 3.4.24.-) 2 - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #ext\_change 20-Sep-1999  
C/Accession: I46078  
R/Emoto, N.; Yanagisawa, M.  
J. Biol. Chem. 270, 15262-15268, 1995  
A/Title: Endothelin-converting enzyme-2 is a membrane-bound, phosphoramidon-sensitive me  
A/Reference number: A57042; MUID:95318093; PMID:7797512  
A/Accession: I46078  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-825 <EMO>  
A/Cross-References: EMBL:U7341; NID:9897599; PID:9897600  
A/Genetics:  
A/Gene: ECE-2  
A/Superfamily: neprilysin  
C/Keywords: hydrolase; metalloproteinase

Query Match	85.5%; Score 3662; DB 2; Length 825;
Best Local Similarity	93.0%; Pred. No. 2.7e-241;
Matches	690; Conservative 22; Mismatches 28; Indels 2; Gaps 1;
QY	70 WRYTCEPHLRISIGLCRTWVGQKGTROLGSRTOLEVLTAASLLALAGCVLALGV 129
DB	86 WTVSSRGVATVQVINE--AGFRKRTSRILGHTOLEVLTAAGVSLALAGCVLALGV 143
QY	130 QYHRDPSHTCLTEACIRYAGKILSLDGVSPCEDYQFSGCGMIRRPDPGRSRWNT 189
DB	144 QYHRDPSHTCLTEACIRYAGKILSLDGVSPCEDYQFSGCGMIRRPDPGRSRWNT 203
QY	190 FNSLWDONALIKHLENTFNSSSEAEQKTFYLSCLQVERIEELGAQPLRLDIETKG 249
DB	204 SLSLWDONALIKHLENTFNSSSEAEKTRFYLSCQVERIEELGAHRLDLIDKIG 263
QY	250 GNNITGPMQDNFMELKAVAGTYRATPFTYIISADSSNSNYIYQVDSGLFLPSRY 309
DB	264 GNNITGPMQDNFMELKAVAGTYRATPFTYIISADSSNSNYIYQVDSGLFLPSRY 323
QY	310 YNRTANEKVLRAVDYMEELGMLGGRPTSRQMOQVLELEIOLANTTVQDORRDE 369
DB	324 YNRTANEKVLRAVDYMEELGMLGGRPTSRQMOQVLELEIOLANTTVQDORRDE 383
QY	370 KYHKMSISELQALAPSDMLEFLSLPSELSDSEPVVYVGYMDYLQGVSELINTEPS 429
DB	384 KYHKMSIAELQALAPSDMLEFLSLPSELSDSEPVVYVGYMDYLQGVSELINTEPS 443
QY	430 IYNTYLINLVOKTSSLDPRFESAQKLETLVGTAKSCVRRNOTCISNTDAGFALG 489
DB	444 IYNTYLINLVOKTSSLDPRFESAQKLETLVGTAKSCVRRNOTCISNTDAGFALG 503



F:591.595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

Query Match 60.4%; Score 2586.5; DB 2; Length 754;

Best Local Similarity 59.9%; Pred. No. 4.6e-168; Matches 479; Conservative 122; Mismatches 151; Indels 47; Gaps 5;

```
14 MVEYKATLDEDEAPETPEVGASPDAMEVKGKSPSPGSPGMPGTPTSSGLFPMRY 73
2 MSYKATLDEDELDVLSBGDYVPNGLQNF-----RSRSQGRCH--- 43
74 CPHLSISGLCSRTWVGOKTRQLGSRTOLEVLVAGSLALLALLGLVALGVGYHR 133
44 -----AARTSEKRLVVLVTLAAGLVACLAVALGIQY-R 76
134 DPHSHSTCLTEACIRVAKKILESIDRGVSPCEDFYQSGGWIRNPLPDGRSRNNTFN 191
77 TRTPPVCLTEACVSVTSILNSMDPTVDPQDFFYACGWIKANPVPDGHSRWGTFSNL 136
194 WDQNOAILKHLLENTTSSSEAEOKTORFYLSCLOVERIEEIGAOPLRLIEKIGGMNI 253
137 WEHQAILIKHLLENST-ASASEAEKKAQVYVRAQMETRIIEELRAKPLMELIEKIGGMNI 195
254 TGEWODNEMEVKAVAGTYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYLYNR 313
196 TGEWADNFDQTLQVTAHYRTSPFVSIVYASDKSSNSNVIOVDSGLFLPSRDYLYNK 255
314 TANBKVLTAIYDIMEELGMLL-CGRPTSTREKQVLELEIOLANTIVPDORDEEKY 372
256 TEHEKVLTYGLNVMVQGLKGDESDIRPQOQIIDFETALANTITIPQKRDEELIY 315
373 HKMSISELOALAPBMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPESILN 432
316 HKTAELQTLAIAINMLPFLNATFYVEINESEPIVYKELIRQVSTILNSTDKCLN 375
433 NYLIMLVOKTSSLDLRRFESAQEKLETLTYGTKSCVPRMOTCISNTDALGFALGSLF 492
376 NYMMMLVKTSSFLDQRFQADAEKFEVVMYGTCTCLPRKFCVSPSTENNLGFALGPMF 435
493 VKATPDRQSEKIEAGMISEIRTAPEEALGOLVWMDKETRQAAEKADAIYDMIGPDPF 550
436 VKATPDRQSEKIEAGMISEIRTAPEEALGOLVWMDKETRQAAEKADAIYDMIGPDPF 550
553 EPEKELDVYDGYEISEDSFQNMNLNYPFSAKVMADOLRKPRSDQMSMTPTQVNAVYLP 612
496 DPEKELDVYDGYEISEDSFQNMNLNYPFSAKVMADOLRKPRSDQMSMTPTQVNAVYLP 612
613 TKNEIVPAGILQAPFYARNHPKALNFGGIGVWVGHETLTHAFDQGREYDEKGLRPMWQ 672
556 TKNEIVPAGILQAPFYARNHPKALNFGGIGVWVGHETLTHAFDQGREYDEKGLRPMWQ 672
673 NBSLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGIKAAVYAYQWVVKNGA 675
616 NSSVEAFKQGTACVBEQVYVNGEVRNGRHTLGENIADNGIKAAVYAYQWVVKNGA 675
733 EQQLPAVGLTNHQLPFGVGAQWCVTPPSSHGVLTPDHPSPARFVYLTLSNSRDEL 792
676 EQQLPAVGLTNHQLPFGVGAQWCVTPPSSHGVLTPDHPSPARFVYLTLSNSRDEL 792
793 HFGCPVSPMNPQOLCEVW 811
736 HFGCPVSPMNPQOLCEVW 754
```

RESULT 4  
S47268  
endothelin-converting enzyme (EC 3.4.24.-) 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:Accession: S51010; S47268  
R:Schmidt, M.; Kroege, B.; Jacob, E.; Seuburger, H.; Subkowski, T.; Otter, R.; Meyer,  
FBS Lett. 356, 238-243, 1994  
A>Title: Molecular characterization of human and bovine endothelin converting enzyme (EC

A:Reference number: S51009; MWID:95104423; PMID:7805846  
A:Accession: S51010  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <SC2>  
A:Cross-references: EMBL:235306; NID:9535074; PIDN:CAA84547.1; PID:9535075  
C:Superfamily: neprilysin  
C:Keywords: hydrolase; metalloproteinase; zinc  
F:591.595/Binding site: zinc, catalytic (His) #status predicted  
F:592/Active site: Glu #status predicted

Query Match 60.0%; Score 2567.5; DB 2; Length 754;

Best Local Similarity 59.6%; Pred. No. 9.2e-167; Matches 477; Conservative 119; Mismatches 154; Indels 51; Gaps 7;

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14 MVEYKATLDEDEAPETPEVGASPDAMEVKGKSPSPGSPGMPGTPTSSGLFPMRY 72
2 MSYKATLDEDELDVLSBGDYVPNGLQNF-----PRNGRCW--- 43
73 CPHLSISGLCSRTWVGOKTRQLGSRTOLEVLVAGSLALLALLGLVALGVGYHR 132
44 -----AARTSEKRLVVLVTLAAGLVACLAVALGIQY 76
133 -RDPHSTCLTEACIRVAKKILESIDRGVSPCEDFYQSGGWIRNPLPDGRSRNNTFN 191
77 TRTP--SVCLSEACISVTSILNSMDPTVDPQDFFYACGWIKANPVPDGHSRWGTFS 134
192 SLMDQOAILKHLLENTTSSSEAEOKTORFYLSCLOVERIEEIGAOPLRLIEKIGGMNI 251
135 NMHEHQAILIKHLLENST-ASVSEAEKKAQVYVRAQMETRIIEELRAKPLMELIEKIGGMNI 193
252 NITGPMDOENMEVKAAGTYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYLY 311
194 NITGPMDOENMEVKAAGTYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYLY 311
312 NITGPMDOENMEVKAAGTYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYLY 311
254 NITGPMDOENMEVKAAGTYRATPFTVYISADSKSSNSNVIOVDSGLFLPSRDYLY 311
371 IYHKMSISELOALAPBMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPESILN 430
314 IYHKMSISELOALAPBMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPESILN 430
431 IYHKMSISELOALAPBMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPESILN 430
374 IYHKMSISELOALAPBMDLEFLSFLSPLESDSEPVVYVGM DYLOQVSELINRTPESILN 430
491 LEVKATPDRQSEKIEAGMISEIRTAPEEALGOLVWMDKETRQAAEKADAIYDMIGPDPF 550
434 LEVKATPDRQSEKIEAGMISEIRTAPEEALGOLVWMDKETRQAAEKADAIYDMIGPDPF 550
551 ILEPEKELDVYDGYEISEDSFQNMNLNYPFSAKVMADOLRKPRSDQMSMTPTQVNAVYLP 610
494 ILEPEKELDVYDGYEISEDSFQNMNLNYPFSAKVMADOLRKPRSDQMSMTPTQVNAVYLP 610
611 LPTKNEIVPAGILQAPFYARNHPKALNFGGIGVWVGHETLTHAFDQGREYDEKGLRPMWQ 670
554 LPTKNEIVPAGILQAPFYARNHPKALNFGGIGVWVGHETLTHAFDQGREYDEKGLRPMWQ 670
671 WONESLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGIKAAVYAYQWVVKNGA 675
614 WONESLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENTADNGIKAAVYAYQWVVKNGA 675
731 GBEQQLPAVGLTNHQLPFGVGAQWCVTPPSSHGVLTPDHPSPARFVYLTLSNSRDE 790
674 GBEQQLPAVGLTNHQLPFGVGAQWCVTPPSSHGVLTPDHPSPARFVYLTLSNSRDE 790
791 LNHFGCPVSPMNPQOLCEVW 811
734 LNHFGCPVSPMNPQOLCEVW 754
```

RESULT 5

JC2521  
endothelin converting enzyme (EC 3.4.24.-) 1, umbilical vein endothelial cell form - hum  
C/Species: Homo sapiens (man)  
C/Date: 17-May-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
C/Accession: JC2521  
R/Shimada, K.; Matsushita, Y.; Wakabayashi, K.; Takahashi, M.; Matsubara, A.; Iijima, Y.  
Biochem. Biophys. Res. Commun. 207, 807-812, 1995  
A/Title: Cloning and functional expression of human endothelin-converting enzyme cDNA.  
A/Reference number: JC2521; MUID:95169126; PMID:7664876  
A/Accession: JC2521  
A/Molecule type: mRNA  
A/Residues: 1-758 <SH1>  
A/Cross-references: GB:D43698; NID:g1197803; PIDN:BA07800.1; PID:g1197804  
A/Experimental source: umbilical vein endothelial cells  
C/Genetics: GDB:ECEL; ECE  
A/Gene: GDB:698357; OMIM:600423  
A/Cross-references: GDB:698357; OMIM:600423  
A/Map position: 1p36.1-1p36.1  
C/Superfamily: neprilysin  
C/Keywords: alternative splicing; glycoprotein; hydrolase; metalloproteinase; transmembr  
P:57-77/Domain: transmembrane #status predicted <TM>  
F:154,175,198,258,304,350,371,527,620,639/Binding site: carbohydrate (Asn) (covalent) #  
F:595,599/Binding site: zinc, catalytic (His) #status predicted  
F:596/Active site: Glu #status predicted

Query Match 59.8%; Score 2561; DB 2; Length 758;  
Best Local Similarity 60.7%; Pred. No. 2,6e-166; Mismatches 150; Indels 34; Gaps 9;  
Matches 477; Conservative 125; Mismatches 150; Indels 34; Gaps 9;  
31 PVEGASPDAMEVKGKASPPSPGP-SFGMTPTGTPRSSGGLFWRYTCPLHRSISGLCRSTW 89  
2 PLOG-----IGLQNPFLQKGRGRLSSPP-----LLPELQ-----Y 35  
90 GFG-KETROLASRTQLEVLVLAGSLLAALLGLVALGVYH-RDPSHSITCTEACT 146  
36 NFHSPPSGRCMAFTQVEKRLVVLVLLAGVACAAAGIOYQTRSP--SYCLSEACV 93  
147 RVAGKLTLESIDRGVSPCEDFYQSCGGMIRNPLPDGRSMWTFNSIMDONAILKHLE 206  
94 SVTSSILSSMDPTVDPCHDFPSTACGMKIANPVDPDHSWGTFSNMEHQAIIKHLE 153  
207 NTTFNSSSEAEOKTQRFYSLQOVERIEELGAOPLRLDIKIGMNTGCPMDNFEVL 266  
154 NSI-ASVSEAEKRAQVYRAQMETRIEELRAKPIELIRLGSWNTGMAWDNPDL 212  
267 KAVAGTYRATPFTFTVYISADSKSSNSNVIOVDSGLFLPSRDYLLNRTANEKYLTA 326  
213 QVTAHRTSPFSSVVSADSKSSNSNVIOVDSGLFLPSRDYLLNRTANEKYLTA 272  
327 MEELGML-GGRPTSTEQMOVLELEIOLANTVPODORDEKTYHKMSISELQALP 385  
273 MVQGLKLGSGDEBALPQOQILDEFETALANTITPEKRRDELIYHKAATAELQTLAP 332  
386 SMDLEFLSLSLSELSDEPVVYVGMVYLAQVSELEINRTEPSILNNYLLNVLVOKTS 445  
333 AIIWMLPELNTIPVVEINSEPIVVDKEYLEQISTLINTDCLANNYIMLVKRTSS 392  
446 SLDRPESAOBKLETLITKSKSCVPRWQTCISTDIALPAGLSLFVKAFTPDROKELA 505  
393 FLIDRFODADEKFMENVYGTAKTCLPRMKCVSDTENNLGFALGPMVKAFTFEDSISA 452  
506 EGMISELIRPEELIQLVMDDEKTRQAKKADAIYDMIGPDPLEPELDDYDGE 555  
453 TEILLETIKKAFEESSLTKMDETRKSAKADAIYDMIGPDPLEPELDDYDGE 512  
566 ISEDSFQNNMLNTNFAKVAWADLRKPSRDQSMPTQTVNAVYUPTKKEIVFPAIIG 625  
513 AVVDLYENMRRPFNFSWRVTAQDLRAKPRDQSMPTPMVNAVYSTKKEIVFPAIIG 572  
626 APFYARNHPALNFGIGVVMGHELTAFDDQGREYDKEGNLRPMWONESLAAPRNATAC 665  
573 APFYTRSSPALNFGIGVVMGHELTAFDDQGREYDKEGNLRPMWONESLAAPRNATAC 632

QY 686 MEEQYNQVNGERLNGRQTLGENTADNGGLKAAVNAVAMLRKKEEQOLPAVGLTNHQ 745  
DB 633 MEOQSYNSVNGEPNVRGRTLLGENTADNGGLKAAVNAVAMLRKKEEQOLPAVGLTNHQ 692  
QY 746 LFFVGAQVWCVSRTPRESSHEGLVTDPSPARFVLTLSNRDPLRHFGCPVSPMNG 805  
DB 693 LFFLGAQVWCVSRTPRESSHEGLVTDPSPARFVLTLSNRDPLRHFGCPVSPMNG 752  
QY 806 QUCQEW 811  
DB 753 HKCEWA 758

## RESULT 6

endothelin converting enzyme (EC 3.4.24.-) 1 - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Nov-1999  
C/Accession: A54667; JC2448  
R/Xu, D.; Emoto, N.; Giald, A.; Slaughter, C.; Kaw, S.; dewlt, D.; Yanagisawa, M.  
Cell 78, 473-485, 1994  
A/Title: ECE-1: a membrane-bound metalloprotease that catalyzes the proteolytic activati  
A/Reference number: A54667; MUID:94340737; PMID:8062389  
A/Accession: A54667  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-758 <XUA>  
A/Cross-references: GB:U27342; NID:9897601; PIDN:AA82928.1; PID:9897602  
R/Ikuta, T.; Sawamura, T.; Shitaki, T.; Hosokawa, H.; Kido, T.; Hoshikawa, H.; Shimada,  
Biochem. Biophys. Res. Commun. 203, 1417-1422, 1994  
A/Title: cDNA cloning and expression of bovine endothelin converting enzyme.  
A/Reference number: JC2448; MUID:95032010; PMID:7945289  
A/Accession: JC2448  
A/Molecule type: mRNA  
A/Residues: 1-90, 'A', 92-698, 'A', 700-758 <IKU>  
A/Cross-references: GB:S73774; NID:9688289; PIDN:AA832062.1; PID:9688290  
C/Superfamily: neprilysin  
C/Keywords: hydrolase; metalloproteinase; transmembrane protein; zinc  
P:57-77/Domain: transmembrane #status predicted <TM>  
F:595,599/Binding site: zinc, catalytic (His) #status predicted  
F:596/Active site: Glu #status predicted

Query Match 59.5%; Score 2546; DB 2; Length 758;  
Best Local Similarity 59.8%; Pred. No. 2,7e-165;  
Matches 474; Conservative 118; Mismatches 160; Indels 40; Gaps 7;  
23 RDEDAETP-VEGASPDAMEVKGKASPPSPGP-SFGMTPTGTPRSSGGLFWRYTCPLHRSIS 81  
4 RGQDLRLSPDLGSEAP-----GLTSSPRLTPPSQVNRGPRNGRCW----- 47  
82 GLCSRTMVGFGKTRQLGSRQLEVLVLAGSLLAALLGLVALGVYH-RDPSHSITC 140  
48 -----AAKTPVEKRLVVLVLLAALVACAAAGIOYQTRTP--SYC 87  
141 LFEACIRVAGKLTLESIDRGVSPCEDFYQSCGGMIRNPLPDGRSMWTFNSIMDONAI 200  
88 LSEGCISVTSILSSMDPTVDPCHDFPSTACGMKIANPVDPDHSWGTFSNMEHQAIIKHLE 147  
201 LKHLLENTFNSSSEAEOKTQRFYSLQOVERIEELGAOPLRLDIKIGMNTGCPMDN 260  
148 IKHLENT-ASVSEAEKRAQVYRAQMETRIEELRAKPIELIRLGSWNTGMAWDNPDL 206  
261 NFMENVKAVAGTYRATPFTFTVYISADSKSSNSNVIOVDSGLFLPSRDYLLNRTANEKYL 320  
207 NFQDTLQVVTSHYHSPFSSVVSADSKSSNSNVIOVDSGLFLPSRDYLLNRTANEKYL 266  
321 TAYDMEELGMLGGRPTST-REQMOVLELEIOLANTVPODORDEKTYHKMSISE 379  
267 TGLANTMVDGLKLGAGADITRPQOQILDEFETALANTITPEKRRDELIYHKAATAELQTLAP 326  
380 LQALASMDLEFLSLSELSDEPVVYVGMVYLAQVSELEINRTEPSILNNYLLNVLVOKTS 439  
327 LQTLAPALNMLPELNTIPVVEINSEPIVVDKEYLEQISTLINTDCLANNYIMLVKRTSS 386









QY 385 PSMMDLLEFLSLSP--LEISDSPPVYVGM DYLOQVSELINRTEPSILNNYLINWL VOK 442  
 Db 319 KPFMSNFNTEININIQNEBEEVVAPEYLTAKRLTKYSPRDLOINMSRFIND 378  
 QY 443 TTSSLDREPRSAOEKLETLTYGTAKSCVPRMOTCISNTD DALGALGSLFYKATPDROK 502  
 Db 379 LVSSLSRNKESRMAFRKALYGT-TSEIATWRCAVYVGNMENAAGRLVYEAFAFESK 437  
 QY 503 ELAEGMISIRTAFEALQOLVWMDKTRQAAKEXADALYDMIGPDPFL-EPKELDVY 561  
 Db 438 HVEDLDAIQIREVFIQTLDLTMMDKTKKAEKALAKERIGYPPDDITINENKLNNEY 497  
 QY 562 DGEIISEDSPFQNM LNLNFSAKVMA DQLRKPPSDQMSMTPTQVAAVYLTPTKNEIVPA 621  
 Db 498 LELANKEEYEFENIIONLKFSSQSKQAKREKVDDEWISGAAYVNAFSSGRNOIVFA 557  
 QY 622 GILQAPFYARNHPKALNFGIGVVMGHELTTHAFDDQGREYDEKGLRPMWQESLAAPN 681  
 Db 558 GILQPPFPARQSNISLNYGIGVIGHEITHGFDNGRNFKNQDGLVDWMTQOASANNFD 617  
 QY 682 HTRACHEOYNOYQ--VNEERLNGRQTLGENTADNGSLKAAAYNAKARKHGEBOQLA 738  
 Db 618 GQOCVYQYGNFTWDLAAGQHLNGINTLGENIADNGIGQAYRAYQNYKNGEELPBG 677  
 QY 739 VELTNHQLFFVGAQVWCVRTPRESSHGLVTDPHSPARFVLTLSNRDPLRHFGCPV 798  
 Db 678 LDLNHKQLFFLNFQVWCTYRPEYAVNSIKTDVHSPGNFRITIGLQNSAEFADAFHCK 737  
 QY 799 GSPNPGQLCEVW 811  
 Db 738 NSYNPBERKCRVW 750

## RESULT 10

HYBN

neprilysin (EC 3.4.24.11) - rabbit  
 N:Alternate names: CD10; common acute lymphocytic leukemia antigen; endopeptidase 24.11;  
 C:Species: Oryzctolagus cuniculus (domestic rabbit)  
 C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 18-Jun-1999  
 C:Accession: A29451; 146872  
 R:Devault, A.; Lazure, C.; Nault, C.; Le Moual, H.; Seldah, N.G.; Chretien, M.; Kahn, P.  
 EMBO J. 6, 1317-1322, 1987  
 A:Title: Amino acid sequence of rabbit kidney neutral endopeptidase 24.11 (enkephalinase  
 A:Reference number: A29451; MUID:87275825; PMID:2440677  
 A:Accession: A29451  
 A:Molecule type: mRNA  
 A:Residues: 1-751 <DEV>  
 A:Cross-references: EMBL:X05338  
 A:Note: part of this sequence, including the amino end of the mature protein, was confir  
 R:Kahn, P.H.; Powell, J.F.; Beaumont, A.; Roques, B.P.; Mallet, J.J.  
 Biochem. Biophys. Res. Commun. 145, 488-493, 1987  
 A:Title: An antibody purified with a lambda GT11 fusion protein precipitates enkephalin  
 A:Reference number: 146872; MUID:87241544; PMID:3297057  
 A:Accession: 146872  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 207-275 <KAH>  
 A:Cross-references: GB:M15593; NID:G165556; PIDN:AAAS3694.1; PID:G165557  
 C:Comment: This enzyme inactivates a variety of peptide hormones, cleaving on the amino  
 ney.

C:Superfamily: neprilysin

C:Keywords: glycoprotein; hydrolase; metalloproteinase; oligopeptidase; surface antigen;  
 F:2-751/Product: neprilysin status experimental <MA>  
 F:16-73/Region: stop-transfer sequence

F:29-51/Domain: transmembrane #status predicted <TM>  
 F:52-751/Domain: extracellular #status predicted <EXT>  
 F:145-286,312,326/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:585-589/Binding site: zinc (His) #status predicted

F:586/Active site: Glu #status predicted  
 F:629/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 29.7%; Score 1272; DB 1; Length 751;  
 Best Local Similarity 35.6%; Pred. No. 1.8e-78;

Matches 262; Conservative 150; Mismatches 288; Indels 36; Gaps 13;  
 QY 103 TQLELVAGASLTLAALLGLVAGVYHNDPSHSTLTACTICRVACKIIESLDGSP 162  
 Db 25 TPLEISLVLLLVIAV-TWIALYATY---DDGICSDPCISANRLQNMATLBP 79  
 QY 163 CEDFYQSCGQWIRNPLPDGRSMNTFNLSMDQNALIKHLENTFNSSSEAEQTOR 222  
 Db 80 CDFKFAQCGMLKKNVLPETSSRSYNDILRDELVLKQVLQPK-TEDIVAAQAKT 138  
 QY 223 FYLSGLQVERIEELGAQPLRDLIEKIGWNI-TGEWDO-----DNFMEYKAVAGTY 273  
 Db 139 LYRSQVNETALDSRGQFLKLPLVYQMPVATQWEGTYGTSWAEKSIQALNSNYGK 198  
 QY 274 RATPFYTYISADSSNSNYQVDSGLFLPSRQYLRNRANENVLTAYIDYMEGLML 333  
 Db 199 VLINFEVV--GTDDKNSNMHIHIDQPLGIPSRBYCTGTGYKACRAYDFMIAVAKL 256  
 QY 334 L---GGRPTSTR---OMQVLELEIOLANITVPQDORDEBKTYHKMSISELQ----- 381  
 Db 257 IROEGGLPIDENQISVENAKWMELEKETAANATKSEDRNDPMLYNKTLAQIONNFSLE 316  
 QY 382 ALAPSMDLLEFLSLSPLELS--DSBPVYVGM DYLOQVSELINRTEPSILNNYLINWL 439  
 Db 317 INKPFMSNFNTEININIPNEEDVVAPEYLTAKRLTKYSPRDLOINMSRF 376  
 QY 440 VOKTSSLDREPRSAOEKLETLTYGTAKSCVPRMOTCISNTD DALGALGSLFYKATPD 499  
 Db 377 IMDLVSSLSRKYKOSRNARFRAKYGTTSESA-TWIRCAVYVGNMENAAGRLVYEAFAF 435  
 QY 500 QSKELAEGMISIRTAFEALQOLVWMDKTRQAAKEXADALYDMIGPDPFL-EPKELD 558  
 Db 436 ESKHYVEDLIAQIRVFIQTLDLTMMDKTKKAEKALAKERIGYPPDDITINENKLN 495  
 QY 559 DVIDGEIISEDSPFQNM LNLNFSAKVMA DQLRKPPSDQMSMTPTQVAAVYLTPTKNEI 618  
 Db 496 NEYELANKEDYEFENIIONLKFSSQSKQAKREKVDDEWISGAAYVNAFSSGRNOIV 555  
 QY 619 PPAGILQAPFYARNHPKALNFGIGVVMGHELTTHAFDDQGREYDEKGLRPMWQESLA 678  
 Db 556 PPAGILQPPFPARQSNISLNYGIGVIGHEITHGFDNGRNFKNQDGLVDWMTQOASANN 615  
 QY 679 FPNHTRACHEOYNOYQ--VNEERLNGRQTLGENTADNGSLKAAAYNAKARKHGEBOQ 735  
 Db 616 FKESQCVYQYGNFTWDLAAGQHLNGINTLGENIADNGIGQAYRAYQNYKNGEELPBG 675  
 QY 736 LPVAGLTNHLFFVGAQVWCVRTPRESSHGLVTDPHSPARFVLTLSNRDPLRHFG 795  
 Db 676 LPGLDNLHKQLFFLNFQVWCTYRPEYAVNSIKTDVHSPGNFRITIGLQNSAEFADAF 735

## RESULT 11

T20003

hypothetical protein ZK20.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
 C:Accession: T20003; T27775

R:Gajdety, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z19209

A:Accession: T20003  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-766 <NII>  
 A:Cross-references: EMBL:Z69902; PIDN:CAA33770.1; GSPDB:GN00020; CESP:ZK20.6  
 A:Experimental source: clone C47D12

R:Gajdety, S.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z20417



## RESULT 13

C88099  
protein F18A12.8 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: C88099  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; WMD:199069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: C88099  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-590 <STO>  
A:Cross-references: GB:chr\_11; PIDN:AB66079.1; PID:g2315629; GSPDB:GN00020; CESP:F18A12.  
C:Genetics:  
A:Gene: F18A12.8  
A:Map position: 2

Query Match 26.2%; Score 1122.5; DB 2; Length 590;  
Best Local Similarity 38.7%; Pred. No. 1.9e-68;  
Matches 229; Conservative 122; Mismatches 220; Indels 21; Gaps 11;

QY 239 QPRLDIKIKGNGNTGP-WDDP--NFMEYLKAVAGTTRATPTPTTYISADSKSSSNVY 295  
DB 1 RPLFETLTELGEWPLLOEWMWDKTFNFSTLVSRRDYGVDFFOLYIYADSKNTSRNTL 60  
QY 296 QVDSGLPL--PSRDYLYNRANETKYLTAVIDMEELGML--GGRPTSRBOM----QQ 347  
DB 61 FIDOSTLALGRGTRDYLLMTTFLSSHMTAYRKTLRQIAHLKTDGULTSESSEMMADIEK 120  
QY 348 VLELEIQLANITVPQDQRDEEKIYHKMSISELQALAPSMDEFLSFLSPLELS---- 403  
DB 121 IDFELELAKIYAEDERRNNTLYNKRODLYNLPOVDWVPFQ-SIAPEDLHLHFI 179  
QY 404 DSEPVVYVGMVYLOVSELIINTEPSILANNYLIMLVQKTTSSLDRPFSAGKLETTY 463  
DB 180 NTEFIIICEIEYLOHVSSELIKTDVGLTNVYLMRVQSNVRYLDERFEDIKODFLKVMY 239  
QY 464 GTRKSCVPRMOCISTDIALGFLGSLVYKATFDSQSEIAEGMISEIRTAEEALGQL 523  
DB 240 GGOQOS--PRFWKCAQVPSVTLPLAAGATVYQAFQSDGHEALRMIMHILKNSADLVKRN 298  
QY 524 VMDEKTRQAAKEKADAIYDMIGFPDPILEPKELDVIDYGEISE--DSEFQNNLANYFS 582  
DB 299 DMNDEETKVAIEKANSMTNINIGYPRVTDLPRLDKQYLGSLSDSDTYIYIMKSVVM 358  
QY 583 AKVMADQLKPPSRDQSMTPQTQVNAVYLPKNEIYFPAIGILOAPYARNHPKALNFGGI 642  
DB 359 OSREFOKLTRPKHEFDISPAVVNAFYSPBKNAITFPAGIILQPPFSGTFPQAVVYGA 418  
QY 643 GYVMGHELTHAFPDQREYDKESGNLAPMONEISLAFRNHTACMEQVNOYOV--NGEKL 700  
DB 419 GAVTGHETIHGFDDQSQYDKDGNLNMWSESLNFDTRRRCTIVQYGNVYTPKTNFR 478  
QY 701 NGRQTLGENIADNGGLKAAVNAKAMLRKKGEEQQLPAV--GLTNHOLEFVGFQAVQVCSVR 759  
DB 479 NGLTQGENIADNGVYKEAFQAKQVYTNNGEPRRLPGILOQYTNBEILFVTSVAHFPQCGK 538  
QY 760 TPBSSHEGLVTDHPSPARFRVIGTLSNSRDLNHFCCPVGSPMNPQQLCEVW 811  
DB 539 KEAAMAOQVLTDBHSPEVFRVIGTLSNMQAFADVVCPRNAPVNPDKICVW 590

## RESULT 14

T24949  
hypothetical protein T16A9.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000

C:Accession: T24949  
R:McMurray, A.  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z19955  
A:Accession: T24949  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-769 <MIL>  
A:Cross-references: EMBL:Z77135; PIDN:CA000879.1; GSPDB:GN00023; CESP:T16A9.4  
A:Experimental source: clone T16A9  
C:Genetics:  
A:Gene: CESP:T16A9.4  
A:Map position: 5  
A:Insertion: 15/2; 59/1; 105/3; 202/1; 336/3; 371/3; 393/1; 424/2; 457/3; 571/1; 637/2; 67  
C:Superfamily: nep1lysin

Query Match 23.2%; Score 994.5; DB 2; Length 769;  
Best Local Similarity 31.2%; Pred. No. 1.5e-59;  
Matches 239; Conservative 153; Mismatches 313; Indels 61; Gaps 19;

QY 96 RDLGSRQLE-LVLAGASLILALLGLVVALG----- 129  
DB 15 RSCLESLTLETLTLPLGLITALLSVLEMLWLDGYKFTDGRPIYPLPFBNSSAVV 74  
QY 130 ----GYHRDPSHSTCTTEACIRVAGKILESIDRGVSPCEDFYQFSCGGMIRNPLPDGRS 185  
DB 75 DRSAGNHD---VCTSRQCVRLAGFLAENLNSKINPCEDFYEFAGVGNGLNKLPAKRP 131  
QY 186 RNNTNSLMDQNALIKELLENTTNSSEAEQKQRFYLSCLQVERIEELGAQPLRDLI 245  
DB 132 LRHTISDVQSRINKQVSKMSLOSPISANEKPMQKAKGYQKCLDEBELESTGEAMRDIA 191  
QY 246 EKIGGM-NITG---PMQDNFMEYLKAVAGTTRATPTPTTYISADSKSSSNVYQVDS 300  
DB 192 KRIQGPFLTEGDKQWQESHWSWEEQALVNLGVNAVILLEMVATDPPSSSSSVLELDP 251  
QY 301 GLFLPSRDYLYNRANETKYLTAVIDMEELGMLGGRPTSTRBOMQVLELEIQLANITV 360  
DB 252 KMGAGSRYYLS--GANDPMLRNYTTLKMTVALGADRALAKENMEAPFLKLVNPSA 310  
QY 361 PODQRDEEKIYHKMSISELQALAPSMDEFLSFLSPL--ELSDSEPVVYVGMVYLOOV 419  
DB 311 DMVRRDPRGNRRRELQKSVFPPIFEKLYKTVKELVALSPNHVTIYVEIDYFVGI 370  
QY 420 SELINTEPSILANNYLIMLVQKTTSSLDRPFSAGKLE---TLYGKSKCVPR--RMQT 475  
DB 371 QHVLQSTPRQVLANIYISRLVQGFSPFLP---PSARBPYQPKANQOTGMFNSPPPDQMED 427  
QY 476 CISNTDDALGFLGSLFVYKATF--DROSKIEAGMISEIRTAEEALGQLVMDEKTRQ 533  
DB 428 CVTLISVIMDMVGLFVENFPEKRAKAKMTE-LTSYIAKEFFIQHVLDMDEITRRR 486  
QY 534 AKEKADAIYDMIGFPDPILEPKELDVIDYGEISEDSFQNN--LNLNFSAKVADQL 590  
DB 487 AISKANMIEYKGFPMVLFNDTWMKMW--GMIIKREYLIHLTIKVLRFTEELL--RL 543  
QY 591 RKPSPRDQSMTPQTQVNAVYLPKNEIYFPAIGILOAPYARNHPKALNFGGI 650  
DB 544 DQPLDRSMWFQSPQAVDVAIYAPNNNEMIFPAGIMOPFLTGLVPPVITYYGAVGAVIGHV 603  
QY 651 THAFDDQGEYVKEGNLAPMONEISLAFRNHTACMEQV--NQOVNGE--RLNGRQTLGE 708  
DB 604 SHAFDDQGOYVEMGNLDMDALEBEKFIETKTRFVQYEVNHYVEADILHNGQLSLGE 663  
QY 709 NIADNGGLKAAVNAKAMLRKKG--EQQLPAV--GLTNHOLEFVGFQAVQVCSVRTPSSSH 765  
DB 664 NIADNGVYKTAFAVNAKAMKSNNTGISSEPALPQFOFTSQOMFFLAYANNMGSILVPRKVI 723  
QY 766 EGLVTDHPSPARFRVIGTLSNSRDLNHFCCPVGSPMNPQQLCEVW 811  
DB 724 QILTDVHAPSKYRAMIPLONNPEFAKAFQCPISGPMNPERKQVW 769



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 19:32:41 ; Search time 18 Seconds

(without alignments)  
2346.050 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSPPMNGQLCEWV 811

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3620	89.2	787	1 ECE2_HUMAN	O60344 homo sapien
2	3662	85.5	787	1 ECE2_BOVIN	Q10711 bos taurus
3	2592.5	60.6	770	1 ECE1_HUMAN	P42892 homo sapien
4	2567.5	60.0	754	1 ECE1_BOVIN	P42891 bos taurus
5	2556.5	59.7	762	1 ECE1_RAT	P42893 rattus norv
6	2538.5	59.3	754	1 ECE1_CAVPO	P97733 cavia porce
7	1407.5	32.9	775	1 ECE1_RAT	Q9J113 rattus norv
8	1395.5	32.6	775	1 ECE1_MOUSE	Q9J110 mus musculu
9	1389	32.4	775	1 ECE1_HUMAN	O95672 homo sapien
10	1283.5	30.0	749	1 NEP_MOUSE	O61391 mus musculu
11	1282.5	30.0	749	1 NEP_HUMAN	P08443 homo sapien
12	1276.5	29.8	749	1 NEP_RABIT	P08049 oryctolagus
13	1272.5	29.7	749	1 NEP_RAT	P07861 rattus norv
14	1272.5	29.4	749	1 PEX_HUMAN	P78562 homo sapien
15	1207	28.2	749	1 PEX_MOUSE	P70659 mus musculu
16	994.5	23.2	769	1 YCWL_CAEEL	Q22523 caenorhabdi
17	960.5	22.4	732	1 KEHL_HUMAN	P23776 homo sapien
18	583	13.6	647	1 PEPO_LACHE	O52071 lactobacilli
19	550	12.8	626	1 PEPO_LACLA	Q07744 lactococcus
20	545	12.7	626	1 YSC6_LACLC	Q09145 lactococcus
21	513	12.0	564	1 YSC6_STRGC	P42359 streptococc
22	135.5	3.2	1159	1 SOR2_HUMAN	O96600 homo sapien
23	124.5	2.9	4128	1 PRKD_HUMAN	P78527 homo sapien
24	124	2.9	1290	1 SMC4_XENLA	P50532 xenopus lae
25	124	2.9	2376	1 TAO3_YEAST	P40468 saccharomyc
26	123.5	2.9	1181	1 CIAE_BACTL	Q03748 bacillus th
27	121	2.8	2273	1 HPA1_YEAST	P32874 saccharomyc
28	120.5	2.8	680	1 OPDA_SALTY	P27377 salmonella
29	120	2.8	936	1 MSH4_HUMAN	O15457 homo sapien
30	119.5	2.8	1581	1 LMG3_MOUSE	Q97066 mus musculu
31	118	2.8	601	1 CY6S1_BUCAI	P57570 buchiera ap
32	116.5	2.7	709	1 HS82_YEAST	P02829 saccharomyc
33	116.5	2.7	1919	1 HAPI_YEAST	P97924 rattus norv

34	115	2.7	514	1 VLI_HPV08	P06417 human papil
35	115	2.7	1060	1 DPJ3_LACLA	Q9c170 lactococcus
36	115	2.7	3038	1 TRIO_HUMAN	O75962 homo sapien
37	114.5	2.7	705	1 YNP2_CAEEL	P34562 caenorhabdi
38	114.5	2.7	724	1 HMR_HUMAN	O75330 homo sapien
39	114.5	2.7	3829	1 SACS_HUMAN	Q9n2j4 homo sapien
40	114	2.7	836	1 GYRA_MYCSE	P47250 mycoplasma
41	114	2.7	1649	1 YG44_SCHPO	O60179 schizosacch
42	113.5	2.7	662	1 TRB2_RHISN	P55399 rhizobium s
43	113	2.6	680	1 OPDA_ECOLI	P27298 escherichia
44	111.5	2.6	700	1 HS9C_DICDI	P54651 dictyosteli
45	111.5	2.6	1191	1 LMG2_MOUSE	Q61092 mus musculu

## ALIGNMENTS

RESULT 1

ID	ECCE2_HUMAN	STANDARD:	PRT:	787 AA.
AC	O60344; Q96NX3; Q96NX4;			
DT	30-MAR-2000 (Rel. 39, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).			
GN	ECE2 OR KIA0604.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS A; B AND C).			
RX	MEDLINE=21575691; PubMed=11718899;			
RA	Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,			
RA	Wardson P.A.;			
RT	"Human endothelin converting enzyme-2 (ECE2): characterization of mRNA			
RT	species and chromosomal localization."			
RL	Biochim. Biophys. Acta 1522:46-52(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM B).			
RC	TISSUE=Brain;			
RC	MEDLINE=98290545; PubMed=9628581;			
RA	Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,			
RA	Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. IX.			
RT	The complete sequences of 100 new cDNA clones from brain which can			
RT	code for large proteins in vitro."			
RL	DNA Res. 5:31-39(1998).			
CC	-1- FUNCTION: Converts big endothelin-1 to endothelin-1 (By similarity).			
CC	-1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-			
CC	trp- -val-22 bond in the precursor.			
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=ECE-2A;			
CC	Isoid=O60344-1; Sequence=Displayed;			
CC	Name=ECE-2B;			
CC	Isoid=O60344-2; Sequence=VSP_005508;			
CC	Name=ECE-2C;			
CC	Isoid=O60344-3; Sequence=VSP_005509;			
CC	-1- SIMILARITY: Belongs to peptidase family M13.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL, AF428263; AAL30386.1; -			







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CC EMBL; U27341; AAA82927.1; -  
 DR HSPD; P08473; IDMT.  
 DR GO; GO:0030659; Cytoplasmic vesicle membrane; ISS.  
 DR GO; GO:0016511; Pendothelin-converting enzyme activity; IDA.  
 DR GO; GO:0008270; F-actin binding; ISS.  
 DR GO; GO:0007420; P-kinase development; ISS.  
 DR GO; GO:0010002; P-cardioblast differentiation; ISS.  
 DR GO; GO:0007267; P-cell-cell signaling; ISS.  
 DR GO; GO:0009790; P-embryonic development; TAS.  
 DR GO; GO:0007507; P-heart development; ISS.  
 DR GO; GO:0014866; P-peptide hormone processing; ISS.  
 DR GO; GO:0008277; P-regulation of G-protein coupled receptor pr. . . ; TAS.  
 DR GO; GO:0042310; P-vasoconstriction; TAS.  
 DR InterPro; IPR006025; Pept M Zn BS.  
 DR InterPro; IPR00718; Peptidase\_M13\_N.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 KM Hydrolyase; Metalloprotease; zinc; Glycoprotein; Transmembrane;  
 Signal-anchor.  
 FT DOMAIN 1 82  
 FT TRANSMEM 83 103  
 FT METAL 104 787  
 FT ACT SITE 624 624  
 FT METAL 628 628  
 FT METAL 628 628  
 FT ACT SITE 684 684  
 FT CARBOHYD 164 164  
 FT CARBOHYD 183 183  
 FT CARBOHYD 187 187  
 FT CARBOHYD 228 228  
 FT CARBOHYD 288 288  
 FT CARBOHYD 333 333  
 FT CARBOHYD 400 400  
 FT CARBOHYD 556 556  
 FT CARBOHYD 649 649  
 FT CARBOHYD 657 657  
 SQ SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CRC64;

Query Match 85.5%; Score 3662; DB 1; Length 787;  
 Best Local Similarity 93.0%; Pred. No. 5.9e-238;

Matches 690; Conservative 22; Mismatches 28; Indels 2; Gaps 1;

QY 70 WFTCPHRLRSISGLSRTWVGFOKTRQLLSRTQLELVLAGSLALALGLCVAGV 129  
 DB 48 WTVSSEGVHTVQVINE--AGFRKRTSRLLGLHTQLELVLAGSLALALGLCVAGV 105  
 QY 130 QYHRDPSHSTCLTEACIRVAGKILSLDRGVSPEDEYFQSCGQWIRNPLPDGSRNWT 189  
 DB 106 QYHRDPSHSTCLTEACIRVAGKILSLDRGVSPEDEYFQSCGQWIRNPLPDGSRNWN 165  
 QY 190 FNSLWDONALIKHLENTFNSSFAEKQTRFYVSCIOVRIEELGQPLRIEKG 249  
 DB 166 SNSLWDONALIKHLENTFNSSFAEKQTRFYVSCIOVRIEELGQPLRIEKG 225  
 QY 250 GNNITGPMQDNFMELVKAAGYTRATPEFTYVISAHSKSSNNVIOVQSGFLPSRDY 309  
 DB 226 GNNITGPMQDNFMELVKAAGYTRATPEFTYVISAHSKSSNNVIOVQSGFLPSRDY 285  
 QY 310 YLNRTPANEVLTAYLDYMEELGMLGGRFTSTREOMQVLEIQLANTITVPQDORRDE 369  
 DB 286 YLNRTPANEVLTAYLDYMEELGMLGGRFTSTREOMQVLEIQLANTITVPQDORRDE 345

QY 370 KIYHMSISELOALAPSDMWLEFLSLPLELSDSEPVVYGYMDYLOQVSELINRTPS 429  
 DB 346 KIYHMSIAELQALAPSDMWLEFLSLPLELSDSEPVVYGYMDYLOQVSELINRTPS 405  
 QY 430 ILNNTLNNLVOKTSSLDPRPESQOEULTLVGTCKKSCYPRMOTCISNTDDALGFLG 489  
 DB 406 ILNNTLNNLVOKTSSLDPRPESQOEULTLVGTCKKSCYPRMOTCISNTDDALGFLG 465  
 QY 490 SLFVATKDRDSKEIAEGMISEIRTAPEALGOLVWMDKTRQAKERADAIYDMIGPPD 549  
 DB 466 SLFVATKDRDSKEIAEGMISEIRTAPEALGOLVWMDKTRQAKERADAIYDMIGPPD 525  
 QY 550 FILEKELDDYDYGIEISDESPFQNMNLVNFSAKVMADQLRKPSRDQMSWPTQVAY 609  
 DB 526 FILEKELDDYDYGIEISDESPFQNMNLVNFSAKVMADQLRKPSRDQMSWPTQVAY 585  
 QY 610 YLPTKNEIVFPAGILQAFYARHPKALNFGIGVWGHETLHAFDDGREGYDEKGNLRP 669  
 DB 586 YLPTKNEIVFPAGILQAFYARHPKALNFGIGVWGHETLHAFDDGREGYDEKGNLRP 645  
 QY 670 WMONESLAFRNHTACMEQYNOYVNGERLNGRQTLENTADNGLKAAYNAKMLRK 729  
 DB 646 WMONESLAFRNHTACMEQYNOYVNGERLNGRQTLENTADNGLKAAYNAKMLRK 705  
 QY 730 HGEEOQLPAVGLTNHQLFFVGFPAQVWCSVRTPSSHEGLVTDPHSPARFVLTLSNRD 789  
 DB 706 HGEEOQLPAVGLTNHQLFFVGFPAQVWCSVRTPSSHEGLVTDPHSPARFVLTLSNRD 765  
 QY 790 FLRHFGCVGSPMNPGLCEVW 811  
 DB 766 FLRHFGCVGSPMNPGLCEVW 787

# RESULT 3

EC1\_HUMAN STANDARD; PRT; 770 AA.  
 ID EC1\_HUMAN Q9UQ06; Q9UPF4; Q9UPM4; Q9Y501;  
 AC P42892; Q14217; Q9UQ06; Q9UPF4; Q9UPM4; Q9Y501;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).  
 GN ECEL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OK NCBI\_Taxid:9606;  
 RN [1]  
 RP SEQUENCE OF 7-770 FROM N.A. (ISOFORM B).  
 RC TISSUE=Placenta;  
 RX MEDLINE=95104423; PubMed=7805846;  
 RA Schmidt M., Kroeber B., Jacob B., Seubert H., Subkowaki T.,  
 RA Oller R., Meyer T., Schmalzing G., Hillen H.;  
 RT "Molecular characterization of human and bovine endothelin converting  
 RT enzyme (ECE-1).";  
 RN FEBS Lett. 356:238-243 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RX MEDLINE=95209687; PubMed=7695628;  
 RA Yoritatsu K., Moroi K., Inagaki N., Saito T., Masuda Y.,  
 RA Maesaki T., Seto S., Kimura S.;  
 RT "Cloning and sequencing of a human endothelin converting enzyme in  
 RT renal adenocarcinoma (ACHN) cells producing endothelin-2.";  
 RN Biochem. Biophys. Res. Commun. 208:721-727 (1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM A AND B).  
 RC TISSUE=Placenta;  
 RX MEDLINE=96102029; PubMed=8530372;  
 RA Valdenaire O., Rehrbacher B., Mattei M.-G.;  
 RT "Organization of the gene encoding the human endothelin-converting  
 RT enzyme (ECE-1).";  
 RN J. Biol. Chem. 270:29794-29798 (1995).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).

RA MEDLINE=95169128; PubMed=7864876;  
RA Shimada K., Matsushita Y., Wakabayashi K., Takahashi M., Matsubara A.,  
RA Iijima Y., Tanawa K.,  
RT "Cloning and functional expression of human endothelin-converting  
RT enzyme cDNA."  
RL Biochem. Biophys. Res. Commun. 207:807-812(1995).  
RN (5)  
RP SEQUENCE FROM N.A. (ISOFORM C).  
RC TISSUE=Umbilical vein endothelial cells;  
RA Takayanagi R.,  
RT "Human endothelin-converting enzyme-1c";  
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
RN (6)  
RP SEQUENCE FROM N.A. (ISOFORM B).  
RL Submitted (Jun-1998) to the EMBL/GenBank/DBJ databases.  
RN (7)  
RP SEQUENCE OF 1-132 FROM N.A. (ISOFORM D), AND TISSUE SPECIFICITY.  
RX MEDLINE=99421637; PubMed=10491078;  
RA Valdenaire O., Lepailleur-Enouf D., Egidy G., Thouard A., Barret A.,  
RA Vranckx R., Tougaard C., Michel J.-B.,  
RT "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated  
RT from an additional promoter."  
RL Eur. J. Biochem. 264:341-349(1999).  
RN (8)  
RP SEQUENCE OF 1-103 FROM N.A. (ISOFORM C), FUNCTION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Umbilical vein endothelial cells;  
RX MEDLINE=98060745; PubMed=9396733;  
RA Schweitzer A., Valdenaire O., Neiboeck P., Deuschle U.,  
RA Dumas Mline Edwards J.B., Stumpf J.G., Loeffler B.-M.,  
RT "Human endothelin-converting enzyme (ECE-1): three isoforms with  
RT distinct subcellular localizations."  
RL Biochem. J. 328:871-877(1997).  
RN (9)  
RP SEQUENCE OF 1-46 FROM N.A. (ISOFORM B).  
RA Baguley C.,  
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
RN (10)  
RP SEQUENCE OF 713-770 FROM N.A.  
RA Flowers M.A., Tai S.C., Baluyut C.A., Cheung A.H., Kau C.L.,  
RA Wong G.K.T., Marsden P.A.,  
RT "Characterization of the human endothelin converting enzyme-1 gene  
RT (ECE-1): genomic structure and chromosomal localization."  
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Converts big endothelin-1 to endothelin-1.  
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
CC Trp-Val-22 bond in the precursor.  
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- ENZYME REGULATION: Inhibited by phosphoramidon.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=B;  
CC IsoId=P42892-1; Sequence=Displayed;  
CC Name=A;  
CC IsoId=P42892-2; Sequence=VSP\_005502;  
CC Name=C;  
CC IsoId=P42892-3; Sequence=VSP\_005504;  
CC Name=D;  
CC IsoId=P42892-4; Sequence=VSP\_005503;  
CC -1- TISSUE SPECIFICITY: All isoforms are expressed in umbilical vein  
CC endothelial cells, polynuclear neutrophils, fibroblasts, atrium  
CC cardiomyocytes and ventricles. Isoforms A, B and C are also  
CC expressed in placenta, lung, heart, adrenal gland and  
CC phaeochromocytoma; isoforms A and C in liver, testis and small  
CC intestine; isoform B, C and D in endothelial cells and umbilical  
CC vein smooth muscle cells; isoforms C and D in saphenous vein  
CC cells, and isoform C in kidney.  
CC -1- SIMILARITY: Belongs to peptidase family M13.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC -----  
DR EMBL, 235307; CAA84548.1; ALT\_INIT.  
DR EMBL, D49471; BAA08442.1; -.  
DR EMBL, X91922; CAA63015.1; -.  
DR EMBL, X91923; CAA63015.1; JOINED.  
DR EMBL, X91924; CAA63015.1; JOINED.  
DR EMBL, X91925; CAA63015.1; JOINED.  
DR EMBL, X91926; CAA63015.1; JOINED.  
DR EMBL, X91927; CAA63015.1; JOINED.  
DR EMBL, X91928; CAA63015.1; JOINED.  
DR EMBL, X91929; CAA63015.1; JOINED.  
DR EMBL, X91930; CAA63015.1; JOINED.  
DR EMBL, X91931; CAA63015.1; JOINED.  
DR EMBL, X91932; CAA63015.1; JOINED.  
DR EMBL, X91933; CAA63015.1; JOINED.  
DR EMBL, X91934; CAA63015.1; JOINED.  
DR EMBL, X91935; CAA63015.1; JOINED.  
DR EMBL, X91936; CAA63015.1; JOINED.  
DR EMBL, X91937; CAA63015.1; JOINED.  
DR EMBL, X91938; CAA63015.1; JOINED.  
DR EMBL, X91939; CAA63015.1; JOINED.  
DR EMBL, X91923; CAA63016.1; -.  
DR EMBL, X91924; CAA63016.1; JOINED.  
DR EMBL, X91925; CAA63016.1; JOINED.  
DR EMBL, X91926; CAA63016.1; JOINED.  
DR EMBL, X91927; CAA63016.1; JOINED.  
DR EMBL, X91928; CAA63016.1; JOINED.  
DR EMBL, X91929; CAA63016.1; JOINED.  
DR EMBL, X91930; CAA63016.1; JOINED.  
DR EMBL, X91931; CAA63016.1; JOINED.  
DR EMBL, X91932; CAA63016.1; JOINED.  
DR EMBL, X91933; CAA63016.1; JOINED.  
DR EMBL, X91934; CAA63016.1; JOINED.  
DR EMBL, X91935; CAA63016.1; JOINED.  
DR EMBL, X91936; CAA63016.1; JOINED.  
DR EMBL, X91937; CAA63016.1; JOINED.  
DR EMBL, X91938; CAA63016.1; JOINED.  
DR EMBL, X91939; CAA63016.1; JOINED.  
DR EMBL, D43698; BAA07800.1; -.  
DR EMBL, AB031742; BAA93687.1; -.  
DR EMBL, AL031005; CAA19767.1; -.  
DR EMBL, AJ130828; CAA64644.1; -.  
DR EMBL, X98272; CAA66922.1; -.  
DR EMBL, AL031728; CAA52285.1; -.  
DR EMBL, AF018034; AAD21221.1; -.  
DR PIR, JC2521; JC2521.  
DR PIR, JC4136; JC4136.  
DR HSP, P08473; IDMT.  
DR MEROPS, M13.002; -.  
DR Genew; HGNC:3146; ECE1.  
DR MIM; 600423; -.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.  
DR InterPro; IPR006025; Pept\_M\_zn\_BS.  
DR InterPro; IPR000718; Peptidase\_M13.  
DR InterPro; IPR008753; Peptidase\_M13\_N.  
DR Pfam; PF01431; Peptidase\_M13; I.  
DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
DR PRINTS; PR00786; NEPRILYSIN.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolyse: Metalloprotease; zinc; Glycoprotein; Transmembrane;  
KW Signal-anchor: Alternative splicing; Polymorphism.  
FT DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT FT (POTENTIAL).  
FT DOMAIN 90 770 EXTRACELLULAR (POTENTIAL).

```

FT METAL 607 607 ZINC (CATALYTIC) (BY SIMILARITY)
FT ACT SITE 608 608 BY SIMILARITY.
FT METAL 611 611 ZINC (CATALYTIC) (BY SIMILARITY)
FT METAL 667 667 ZINC (CATALYTIC) (BY SIMILARITY)
FT ACT SITE 671 671 PROTON DONOR (BY SIMILARITY)
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 539 539 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT VARSPLIC 1 44 MAGWPPVPSALLSALGMSYKATLDEEDVDLSLEGAY

Query Match 60.6%; Score 2592.5; DB 1; Length 770;
Best Local Similarity 59.5%; Pred. No. 3,6e-166;
Matches 484; Conservative 124; Mismatches 152; Indels 53; Gaps 7;

1 MNVALQELGAGSNMVEYKATLDEAPETPVEGASPPAMEVGKASFPSPGMP 60
9 VSALLSALG---MSTYKATLDEEDVDLSLEGAYPGLQVNF----- 49
61 GTPRSSGLFWRYTCPLRLSISGLCRITWVGFGKTRQLLSRTOLELVLAGSLIAAL 120
50 HSPRSGQR---AATQVHKRLVVLVLAAGL 80
121 LGLVALGVQYH-RDPSHSTCTEACIRVAGKILSLDRGVSPCEDFYQSGGWIRNP 179
81 VACLAALGIQYOTRSP--SVCLSEACVSTSSILSMDEPTVPCDHFVYACGWIKANP 138
180 LDPGSSRMFTSINDONALIKHLENTFNSSSAEOKTQRFYLSCLQVRIEILAQ 239
139 VPDGHSRMFTSNLMEHNOAIKHLENT-ASVSAERKAVYVYACGWIRIEELRAK 197
240 PLRDLIEKGNWNGNPGMDNFMELKAVAGYRATPEFYIYISADSSNSNYIQVQ 299
198 PLMEILERGWNITGPMKDNFODLVYTAHRYSPFSYVVSADSSNSNYIQVQ 257
300 SGLFPPSRDYLNRTANEKYLTAVIDYMEELGML-GGRPTSTREMOQVLELEIOLANI 358
258 SGLGPPSRDYLNRTANEKYLTAVIDYMEELGML-GGRPTSTREMOQVLELEIOLANI 317
358 TYPQDQRDEEKIYHKMSISEIQAAPSDMTLEPFLSPLELSDSEPVVYVGYMDYLOQ 418
318 TIPOEKRRDEELIYHKVTAELQTLAPAINMLPFLNTIYFPVEINESEBPIVYVDKEYLEQ 377
419 VSELNRTPELILNVLNLTOKTSSLDREPFESAOELTLTYGTSKSCVPRMOTCS 478
378 ISTLNITDRCLNNTMNLVKTSSFLDQRFODDERFMEVMTGKTCCLPRMFCVS 437
479 NTDDALGFLGSLFYVATFPDROSKEIAEGMISEIRTAFEALGOLVWMDKTRQAKEXA 538
438 DIENNGLFLGFMFYKATFAEDSKSATIEIILEIKAFESISTLTKMDEEIRKAKEXA 497
539 DAIVMIGPPDILBEKEIDVYDGEISEDSFPQNTLNLNPSAKVADQLRKPPSRDQ 598
498 DAIVMIGPPDILBEKEIDVYDGEISEDSFPQNTLNLNPSAKVADQLRKPPSRDQ 557
599 WMTPTQTVAAVYLPKNEIVPAGILQAFYARNHPKALNPGIGVGMGHELTTHAPDOG 658
558 WMTPTQTVAAVYLPKNEIVPAGILQAFYARNHPKALNPGIGVGMGHELTTHAPDOG 617
659 REYDEKGLRPMWONESLAFRNHTACMEEOYNOYVNGERLNGRQTLGENTADNGLKA 718
618 REYDEKGLRPMWONESLAFRNHTACMEEOYNOYVNGERLNGRQTLGENTADNGLKA 677
719 AYNAKAMLRKGEBOQLPAVGLTNHQLFFVGPQVQWCVRPESSEHGLVTDPSPARF 778
678 AYNAKAMLRKGEBOQLPAVGLTNHQLFFVGPQVQWCVRPESSEHGLVTDPSPARF 737

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QY 779 RVLGTLNSRDLRFRCGPGVSPMNPQGLCEW 811
DB 738 RVLGTLNSRDLRFRCGPGVSPMNPQGLCEW 770

RESULT 4
BCE1 BOVIN STANDARD; PRT; 754 AA.
ID BCE1 BOVIN
AC P42891;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).
OS BCE1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI TaxID=9913;
RN [1]
RP SEQUENCE FROM N. A., AND PARTIAL SEQUENCE.
RX MEDLINE=95104423; Pubmed=7805846; Seuburger H., Subkowski T.,
RA Schmidt M., Kroege B., Jacob E., Seuburger H., Subkowski T.,
RA Oetler R., Meyer T., Schmalzing G., Hillen H.;
RT "Molecular characterization of human and bovine endothelin converting
RT enzyme (ECE-1).";
RL FEBS Lett. 356:238-243 (1994).
CC -1- FUNCTION: Converts big endothelin-1 to endothelin-1.
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC -1- Tyr-Ile-Val-22 bond in the precursor.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- ENZYME REGULATION: Inhibited by phosphoramidon.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: Belongs to peptidase family M13.
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CC -----
DR EMBL; Z35306; CA884547.1; -.
DR FIR; S51010; S47268.
DR HSP; P08473; IDMT.
DR MEROPS; M13.002; -.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR00718; Peptidase_M13.
DR InterPro; IPR008753; Peptidase_M13_N.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 53 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT METAL 74 754 EXTRACELLULAR (POTENTIAL).
FT ACT SITE 591 592 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 595 595 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 651 651 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 655 655 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 754 AA, 85616 MW, E9276CCCB86FF4C CRC64,  
 Query Match 60.0%; Score 2567.5; DB 1; Length 754;  
 Best Local Similarity 59.6%; Pred. No. 1.7e-164;  
 Matches 477; Conservative 119; Mismatches 154; Indels 51; Gaps 7;

QY 14 MEYKATLRDEPAPETPVEGASPMAMEYG-KGASPFBSGSPGKTPGTSSGCLPMFV 72  
 2 MSTYKRPITDEEDLVSLSESDVYPNHLQVNFGR-----FRAGRCW-- 43  
 DB 73 TCHPLASISGLCRWVGFQKTRQLGSRTOLELVLAGASLLAALLGLCVAGVOH 132  
 44 -----AAATPVEKLVVLAALAAALVACALVGLGIQY 76  
 QY 133 -RDPSTCLTEACIRVAGKILSLDRGVSPCEDFYQSCGWIRRNPLPDGRSMTN 191  
 77 TRTP--SVCLSEACISVTSILSSMDPTVDPCDFTYACGWIKANPVPDGSRMGT 134  
 QY 192 SLWDONQALIKHLENTTNSSEBAQKQRYFLSCLQVERIBELCAOPLRLIEKIGW 251  
 135 NMEHNOAIIKHLENST-ASVSEARKQOEYRACMNTRIELKAKPLMELIEKLGW 193  
 QY 252 NITGPDONFMVAVAGTATPFTYISADSKSSNSVIOVDSGLFLPSRDTL 311  
 194 NITGPDONFMVAVAGTATPFTYISADSKSSNSVIOVDSGLFLPSRDTL 253  
 QY 312 NRTANEKVLAYADYMEELGLGRPTST-REMOQVLELEIOLANITVPODORDEEK 370  
 254 NKTENKVLGYLVNVOGLKGGABEDIRQMOIIDFALANITIPCKRDEEL 313  
 QY 371 IYKMSISELOALPSMDLEPFLSLPSLSDSPPVYVYGMVYQVSELINTEPSI 430  
 314 IYKVAELQTLAPAINMLPFLNTIPYVEINSEPIVYDKEYLSKSTLINSIDKCL 373  
 QY 431 LNNYLVNIVOKTSLDRFESAOKLETTKSKSCVPRQOTISNTDGLFALGS 490  
 374 LNNYLVNIVOKTSLDRFESAOKLETTKSKSCVPRQOTISNTDGLFALGS 433  
 QY 491 LFKATFDRSOSKEIAGMISEIRTAFEALQGLVWDEKTRQAKKADAIYDMIGPDP 550  
 434 MFKATFDRSOSKEIAGMISEIRTAFEALQGLVWDEKTRQAKKADAIYDMIGPDP 493  
 QY 551 ILEPKLADYVYDGEISEDSFFQNMALNYSKAKNADQLRKPSDQMSPTPTNAY 610  
 494 IMPKELDKVFNVDYTPDLVFENAMRFNFSWRVYADQLRKAPNDQMSPTPTNAY 553  
 QY 611 LPTKNEIVPAGILQAPYABRNPKALNFGIGVWGHETLHAFDQGRHYDEKGLRPM 670  
 554 SPKNEIVPAGILQAPYABRNPKALNFGIGVWGHETLHAFDQGRHYDEKGLRPM 613  
 QY 671 WONESLAAPNHTACMEBOYQYQVNGERLNGRQTLGENTADNGLKAAYNAKWLARK 730  
 614 WKNSSVEAFHQOACVBOYGNYSVNGEPVNGRHTIGENIADNGLKAAYNAKWLARK 673  
 QY 731 GEEQOLPANGVLTNHOQPFVGFQAVWCSVTPSSHGLVTDPSPARFVLTLSNRPF 790  
 674 GAEQOTLTGLTNNQFLFLSFAQWCSVTPSSHGLVTDPSPARFVLTLSNRPF 733  
 QY 791 LRHGGCVSGPMNPGQLCEVW 811  
 734 SEHFHCPGSPMNPNNHKEVW 754

RESULT 5  
 ECE1 RAT STANDARD; PRT; 762 AA.  
 AC P42893; Q9WU9; Q9WU9;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECB-1).  
 GN ECE1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid:10116;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORM C).  
 RC TISSUE=Endothelial cells;  
 RX MEDLINE=94308046; PubMed=8034569;  
 RA Shimada K., Takahashi M., Tanzawa K.,  
 RT "Cloning and functional expression of endothelin-converting enzyme  
 from rat endothelial cells."  
 RL J. Biol. Chem. 269:18275-18276(1994).  
 RN [2]  
 RP SEQUENCE OF 1-116 FROM N.A., ALTERNATIVE SPLICING, SUBCELLULAR  
 RC LOCATION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=94421637; PubMed=10491078;  
 RA Valdenaire O., Lepailleur-Enout D., Egidy G., Thouard A., Barret A.,  
 RT "A fourth isoform of endothelin-converting enzyme (ECE-1) is generated  
 from an additional promoter."  
 RL Eur. J. Biochem. 264:341-349(1999).  
 RN [3]  
 RP SEQUENCE OF 1-109 FROM N.A. (ISOFORM A).  
 RC STRAIN=Sprague-Dawley; TISSUE=lung;  
 RX MEDLINE=95402196; PubMed=7672114;  
 RA Shimada K., Takahashi M., Ikeda M., Tanzawa K.,  
 RT "Identification and characterization of two isoforms of an  
 endothelin-converting enzyme-1."  
 RL FEBS Lett. 371:140-144(1995).  
 CC - FUNCTION: Converts big endothelin-1 to endothelin-1.  
 CC - CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-  
 CC tip-1-val-22 bond in the precursor.  
 CC - COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC - ENZYME REGULATION: Inhibited by phosphoramidon (By similarity).  
 CC - SUBUNIT: Homodimer (By similarity).  
 CC - SUBCELLULAR LOCATION: Type II membrane protein.  
 CC - ALTERNATIVE PRODUCTS: Type II membrane protein.  
 CC - Event=Alternative splicing; Named isoforms=4;  
 CC Name=A;  
 CC IsoId=P42893-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=P42893-2; Sequence=VSP\_005505;  
 CC Name=C;  
 CC IsoId=P42893-3; Sequence=VSP\_005506;  
 CC Name=D;  
 CC IsoId=P42893-4; Sequence=VSP\_005507;  
 CC - TISSUE SPECIFICITY: All isoforms are expressed in aortic  
 CC endothelial cells. Isoform A is also expressed in liver; isoform B  
 CC in smooth muscle cells and fibroblasts; isoform C in aortic  
 CC endothelial cells, smooth muscle cells, fibroblasts, liver and  
 CC lung, and isoform D in smooth muscle cells.  
 CC - SIMILARITY: Belongs to peptidase family M13.  
 CC -----  
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 CC -----  
 CC EMBL; D29683; BAA06152.1; -;  
 CC EMBL; AJ130826; CAB46528.1; -;  
 CC EMBL; AJ130827; CAB46529.1; -;  
 CC EMBL; D63795; BAA09864.1; -;  
 CC PIR; A53679; A53679.  
 CC PIR; S66530; S66530.  
 CC HSP; P08473; IDMT.  
 CC MEROPS; M13.002; -;  
 CC InterPro; IPR006025; Pept\_M\_Zn\_BS.

DR	InterPro	IPR000718; Peptidase_M13_N.
DR	InterPro	IPR008753; Peptidase_M13_N.
DR	Pfam	PF01431; Peptidase_M13_1.
DR	Pfam	PF05649; Peptidase_M13_N_1.
DR	PRINTS	PRO0786; NEPRILYSIN.
DR	PROSITE	PS00142; ZINC_PROTEASE; 1.
DR	Hydrolase	Metalloprotease; zinc; Glycoprotein; Transmembrane;
KW	Signal-anchor	Alternative splicing.
KW	Domain	CITOPASMIC (POTENTIAL).
FT	TRANSMEM	1 60 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	82 762 EXTRACELLULAR (POTENTIAL).
FT	METAL	599 599 ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	600 600 BY SIMILARITY.
FT	METAL	603 603 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	659 659 ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	663 663 PROTON DONOR (BY SIMILARITY).
FT	CARBOHYD	158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	VARSPLIC	1 36 MSLRPPQGLGLOMSFFLGGKPGELTVSLPLASS -> M MSYRYALDEEDVLSLSEGDYNG (in isoform C).
FT	VARSPLIC	1 36 MSLRPPQGLGLOMSFFLGGKPGELTVSLPLASS -> M ETLRESVLAALQMSYRYALDEEDVLSLSEGDYNG (in isoform D).
FT	VARSPLIC	1 36 MSLRPPQGLGLOMSFFLGGKPGELTVSLPLASS -> M /FTID=VSP 005507.
FT	SEQUENCE	762 AA; 86125 MW; D688253B67CCAD8 CXC64;
Query Match	Best Local Similarity	59.7%; Score 2556.5; DB 1; Length 762;
Matches	473; Conservative	121; Mismatches 153; Indels 11; Gaps 6;
QY	63	PRSGGLFPR-----VTCPLHR-SISGLCSRTMVGQ--KGRROLIGSTQLELYLAGSL 114
DB	7	PQGLGLQMSFFLGGKPGELTVSLPLASSIQVFRPSRQRCWAARTISVYKRLVVLVT 66
QY	115	LIALLLIGLCTVALGQVYHRDSSHSTCLCEACIRVAGKLTLESIDRGVSCCEPPOPSGGG 174
DB	67	LIAAGLVACIALALGIQY-RTITPPVCLTLEACVSTSSILNSMDPVDPCCQFFSYACGG 125
QY	175	IRRNPLPDGRSRWNTFNSLMDONQALIKHLLLENTFNSSSEAEOKTORFYLISCLQVERIE 234
DB	126	IKANPVPDGRHMRGTFPSNLMEHQIILKHLLENST-ASASEAKKAQYYVRAQMMETRIE 184
QY	235	ELGAPLRLDLLEKIGGNWITGPWODNMEYLKAVAGTYRATPFTTYVTSADSSNSNV 294
DB	185	ELRAKPLMELLLEKIGGNWITGPWADKNQDPTLQVVTATARTSPFSSVYVADSKNSNSV 244
QY	295	IQVQSGGLFSPRDYYLNRTRANEKLTLYVLYMEELGML-CGRTSFRQMOQVLELEI 353
DB	245	IQVQSGGLFSPRDYYLNRTRANEKLTLYVLYMEELGML-CGRTSFRQMOQVLELEI 304
QY	354	QLANITVPQDQRDEKITYRKSISELQALAPSDMEFLISFLLSPLELSDSEPVVYGM 413
DB	305	ALANITTPQERGRDEELIYHKVTAELQTLPAIWMLEPFLNAIFYPVINESEPIVYDK 364
QY	414	DYLQVSLNIRTRTESLNNLTVLWLYVOKTSSILDRPRESAQEKLEFLLVETKYSQVPRW 473
DB	365	EYLQVSLNIRTRTESLNNLTVLWLYVOKTSSILDRPRESAQEKLEFLLVETKYSQVPRW 424

Oy		47	OTCSINDDALGFALGSLPYKATFTDROSKIEAEGMISEIRAPAEALQOLVMDCKTROA	533
Dd		425	KFCVSDBENNIGFPLAGPMFYAKTFAEDSKNTASIIIEIKAFRESISTLTKWMEDETRRS	484
Oy		534	AKEGADAIYIMIGPPDFILSPKELDVVDYGSEISDSFFQMNLNLYNSAKVMADQLRKP	593
Dd		485	AKERADAIYIMIGPNIPTIMPKEIDKXFN DYTAVPDL YFENAMFPNFSLRTVTDQLRKA	544
Oy		594	PSRDQSMTPQTUNAYYLPTKNELIVFPAGILLQAFYARNHPKALNFGSIGVMGHELTTHA	653
Dd		545	PNRDQSMTEPPMVAAYSPTKNELIVEFAGILLQAFYTRSSPNALNFGSIGVMGHELTTHA	604
Oy		654	PDOCGREYDKEGNLRPMWNQNESLIAFRNHRACMEEQNOVOYNGERLINTROTLAGENTADN	713
Dd		605	FDDGRREYDKDNGLRPWMKNSVEAFKQOETECWQQNNYSVNSEPANGRTTGENTADN	664
Oy		714	GGLGAANAAYNAWKMLRKKGESQQLPAVALGTJHOLFVFVFAQVCVARTPESSHEGLVTDPH	773
Dd		665	GGLGAARAARQAQNWKKGAGAILPTLLGLTSNQLPFLLGFAQVCVSRIPESSHEGLITDPH	724
Oy		774	SPAARFVLGTLSNSRDLRFHFQGCVGSPMNPGOLCEVW	811
Dd		725	SPSFRFVIGLSINSKESEHFRCPGLSPMNPBRHCCEVW	762
<hr/>				
RESULT 6				
ID	ECEL_CAVPO	STANDARD;	PRT;	754 AA.
AC	P97739;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
De	Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1).			
GN	ECEL1.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
OX	NCB1 TaxID=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96192242; PubMed=8624482;			
RA	Shima H., Yamanouchi M., Omori K., Sugitara M., Kawashima K.,			
SA	Sato T.;			
RT	"Endothelin-1 production and endothelin converting enzyme expression			
RL	by guinea pig airway epithelial cells.";			
CC	Biochem. Mol. Biol. Int. 37:1001-1010(1995).			
CC	-1- FUNCTION: Converts big endothelin-1 to endothelin-1.			
CC	-1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-			
CC	TP-I-VaI-22 bond in the precursor.			
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).			
CC	-1- ENZYME REGULATION: Inhibited by phosphoramidon (By similarity).			
CC	-1- SUBUNIT: Homodimer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein.			
CC	-1- SIMILARITY: Belongs to peptidase family M3.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	HSPB; S82653; AAB46734.1; --			
DR	HSSP; P08473; IDMT.			
DR	MEROPS; M13_002; --			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR000718; Peptidase_M13.			
DR	InterPro; IPR008753; Peptidase_M13_N.			
DR	Pfam; PF01431; Peptidase_M13; I.			
DR	Pfam; PF05649; Peptidase_M13_N; 1.			
DR	PRINTS; PR00786; NEPRILysin.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1			

KM Hydrolyase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;  
 KM Signal-anchor.  
 FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL)  
 FT TRANSMEM 53 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT  
 FT DOMAIN 74 754 EXTRACELLULAR (POTENTIAL)  
 FT METAL 591 591 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 592 592 BY SIMILARITY.  
 FT METAL 595 595 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 651 651 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 651 651 PROTON DONOR (BY SIMILARITY).  
 FT 655 655 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 754 AA; 85772 MW; F064C57F2BA8A0 CRC64;  
 Query Match 59.3%; Score 2538.5; DB 1; length 754;  
 Best Local Similarity 58.7%; Pred. No. 1.5e-162;  
 Matches 469; Conservative 128; Mismatches 155; Indels 47; Gaps 5;  
 14 MVEYKATLDEDAPEFVPGGASPDAMEYKASPPSPSGMTPTGTRSSGLFMRVT 73  
 2 MSYTKATLDEEDLVSLSGEYVNGLOV----- 31  
 74 CPHLSISGLCSRTMVFQKGTROLGSRQLEVLVLAGSLLAALLGLVALGYOYHR 133  
 32 --NFRN-----RSSQRCATRTQVEKGLIVALLAAGVACLTALGLGY-R 76  
 134 DPHSTCTEACIRVAKILIESLDGVSPCEDFYQSGGWRIRNPLPDGRSWMNTFNSL 193  
 77 TRTPVCLSBACVSVTSILNSMNPVTPDCDFSVACGMIRANPVPDGHSMGAFSNL 136  
 194 WDNOALIKLLENTTNSSEAEQKTRFYLSCTQYERIEELGACPLRLIKIGWNI 253  
 137 WENHOALIKLLENT--ASVSEAEKRAQVYRACMETRIEELRAKLMELIKLGGWNI 195  
 254 TGHMDODNFMVEVKA VAGTRATPTFTVYISADSKSSNSVVIQVDSGLFLPSRDYLYNR 313  
 196 TGHMADNFDQITQVTAHRTSPFESVYVSADSKSNRNVIVHDGSLFLPSRDYLYNR 255  
 314 TANEXVLTAVLYMEELGMLL--GGRPTSTREQVQVLELQIOLANTVPODQRDEKLY 372  
 256 TENEXVLYNTVNVQGLKLGADENAIQAQOQIILDFETALANITIPQEKRRDELY 315  
 373 HKMSISLOALASMDLEFLSLPSLELSDSEPPVYVGMVLOQVSELIINTEBSILN 432  
 316 HKVTAELQVLAIPALNPLPLNATFYVEINESEPIVYVKEYLEQVSTLINTTDCILN 375  
 433 NYILNVLNOKTSLSDRPFESAQKLELTLYTKKSCVPRMOCISINTDGLFALGSLP 492  
 376 NYIIMLVNKRITSSFLDQRFQDADBEKMEVNYGKTKCLPMMKCVSPTENNLGFGLGPM 435  
 493 VKATFROSKEIAEGMISIRTAEEALGQVWMDKTRQAKAEKADAYDMIGPDDIL 552  
 436 VKATFADSDKNIASEITLITKAFEEELSTLKNWDEDTKSAKADAYNMIGPDDIL 495  
 553 EPEKEDLVYDGYEISESFFQNMNLNYSKAKVMAQDLKRPSPRDQSMPTPQVNAVAYLP 612  
 496 DPEKEDLVYDGYEISESFFQNMNLNYSKAKVMAQDLKRPSPRDQSMPTPQVNAVAYLP 555  
 613 TKKEIVFPAGITLAPFARAHNPRALNCGGVVWGHGLTAFPDQDREYDKEGNLPPM 672  
 556 TKKEIVFPAGITLAPFARAHNPRALNCGGVVWGHGLTAFPDQDREYDKEGNLPPM 615  
 673 NESLAAFRNHTACMEQYNOYOVNGERLNGRQLTGENIADNGGLKAAVNAKMLKRG 732

Db 616 NSSVEAFKQOTECMVEQYNSVNGEPVNGRHITLGENIADNGGLKAAVNAKMLKRG 675  
 Qy 733 EQLPAAVGLTNQLFVFGAOWCSVTPRESSHEGLYTDPSPARVYGTLSNSDFLR 792  
 Db 676 EELPLTGLTNQLFVFGAOWCSVTPRESSHEGLYTDPSPARVYGTLSNSDFLR 735  
 Qy 793 HFGCPVGSPPMNPQGLCEW 811  
 Db 736 HFQCPVGSPPMNPQGLCEW 754  
 RESULT 7  
 ECEL RAT STANDARD; PRT; 775 AA.  
 ID ECEL RAT 09JHL3; 09J192;  
 AC 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)  
 DE (Damage-induced neuronal endopeptidase).  
 GN ECEL OR XCE OR DINE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Miscar; TISSUE=Brain;  
 RX MEDLINE=20226106; PubMed=10759559;  
 RA Kikyo-Seo S., Sasaki M., Yokohama H., Nakagami S., Hiyaama T.,  
 RA Aoki S., Wada K., Kiyama H.,  
 RT "Damage-induced neuronal endopeptidase (DINE) is a unique  
 RT metalloproteinase expressed in response to neuronal damage and  
 RT activates superoxide scavengers." Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350 (2000).  
 RL [2]  
 RN SEQUENCE OF 431-632 FROM N.A.  
 RP MEDLINE=99132387; PubMed=9911490;  
 RX Valdenaire O., Richards J.G., Faull R.L.M., Schweizer A.;  
 RT "XCE, a new member of the endothelin-converting enzyme and neutral  
 RT endopeptidase family, is preferentially expressed in the CNS.";  
 RL Brain Res. Mol. Brain Res. 64:211-221(1999).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides. Cleaves  
 CC the synthetic substrate Z-Gly-Gly-Ileu-pNa and releases pNa. May  
 CC protect against C2-ceramide-induced apoptosis.  
 CC -1- COFACTOR: Binds 1 zinc ion (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in  
 CC neurons of the caudate putamen, diagonal band, the paraventricular  
 CC nucleus of the thalamus, part of the hypothalamus, in cranial  
 CC motor nuclei, inferior olive, and substantia nigra.  
 CC spinal tract trigeminal nucleus. Not detected in cerebral cortex,  
 CC hippocampus and cerebellum.  
 CC -1- INDUCTION: By mechanical damage to nerve cells.  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
 CC  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; AB026293; BAA95004.1; -;  
 CC EMBL; AB023896; BAA95006.1; -;  
 CC EMBL; Y16188; CAAT6114.1; -;  
 CC HSSP; P08473; IDMT.  
 CC MEROPS; M13.007; -;  
 CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 CC InterPro; IPR000718; Peptidase\_M13.  
 CC InterPro; IPR008753; Peptidase\_M13\_N.



DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KM Hydrolyase; Protease; Metalloprotease; Metal-binding; Zinc;  
 KW Glycoprotein; Transmembrane; Signal-anchor.  
 FT DOMAIN 1 61  
 FT TRANSMEM 62 82  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT LUMENAL (POTENTIAL).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT\_SITE 612 612  
 FT METAL 613 613  
 FT METAL 616 616  
 FT METAL 672 672  
 FT CARBOHYD 255 255  
 FT CARBOHYD 322 322  
 FT CARBOHYD 656 656  
 FT CONFLICT 536  
 FT SEQUENCE 775 AA; 87944 MW; 0823091F98A41556 CRC64;

Query Match 32.9%; Score 1407.5; DB 1; Length 775;  
 Best Local Similarity 36.8%; Pred. No. 1.3e-86;  
 Matches 299; Conservative 154; Mismatches 291; Indels 69; Gaps 15;

29 ETPVEGASPDAMEVGKASPFSPSPG--MTPTGTRSSGLFWVTCPHLRSIG---- 82  
 2 EAPYSTAHYDERQEVKYSRCCTGARGTSLPFGPRSSG-----RSASGARBG 51  
 83 -----LCSTWVGFKQKTRQLGSRTOLEVLVAGAILLAALLGLVALGVGYHRD 134  
 52 LPRMNRREVCLLSGVFAAGLCALILAMALAKYLGAAGTGAEGACPEG----- 100  
 135 PSHSTCLTACIRVAKILIESLDKGVSPCEDPFGSCGMIRNP.LPDRSKRNTNSLM 194  
 101 PER---FAFAAAFTLSANLDASIDPCQDFSPFACGMRLRHAI.PDKLTYYGTIAAG 155  
 195 DONQALIKHLENTFSSSEAEQKQREYLSCLQVERIEBELGAOPLDLIEKIGMNT 254  
 156 EGNERTLRILARPTGPGGAQRKRAFRSLDMREIERLGRMLLEVIIECGMDIG 215  
 255 GP-----WDQNFMEVILKAVAGTYRATPPTVYISADSKSSNSNVIQVDSGLFSP 306  
 216 GAADRGARWDLN---RLLYKAQGVYSAALFSLTIVSLDDRRNSRYIRIDQGLTPE 272  
 307 RRYLYNR-TANRKYLTAYIDYMEELGMLGRTSTRBEOQVLEHIOQANTVQ--D 363  
 273 RLYLAQDGESEKVLAAVYFMRRLRLGGA--DAVEQAKOELLQLEORLANISVEYD 330  
 364 QRDEEKIYHKMSISEIALAPSMDWLEFLSLPL--ELSDSEPVVYVGGDYQOVS 420  
 331 LRRDVS SVNKTTLGLOKITRHLQ---KWLDDI PQEDSEEEVULATDVIQOVS 386  
 421 ELINRTSPILNNYILNVLQKTTSSLDRRPESAOBKLETTYGTRKSCVPR--WQTCIS 478  
 387 QLRSTPRRLNHYLVWVAVVVLSEHLSPFREALHELAKEMGNDK---PQELAVCG 443  
 479 NTDDALGFLGSLFYVATDROSKEIAEGMISIRAFEBALGQVWDEKTRQAKERA 538  
 444 QANRHFGMLGALFVHEHPSAASKAVQOVLVEDIKYILQOREELDMWMAQTKRAARL 503  
 539 DAIVDMIGPPDFLEBEKLDVYDGEISEDSFQWMLNLVNSAKVAMDOLRKPSRQ 598  
 504 QYMMWVGVGPDPLREAVDKYE-REVEKTYLKRIILNISIRFSLDSYKTKROEVDKT 562  
 599 WMTPTQTVNAYYLLPTNELLVPPAGILQAFYANRHKALNFGSIGVVMGHELTAFDDG 658  
 563 WLLPQALNAYYLLPNQGVVPPAGILQPTLYDDPQOSINYGIGIIGHELTGVDWG 622  
 659 REYDKENLRPMWQNSLAFRNHTCMEEQVQVQVNERLNGRTTGENTADNGLKA 718  
 623 GQYDRSGNLLHWMTENSYSRFLKAECLIVLYDNFTVYQVVGKTTLENTADWGLKL 682  
 719 AVNAYKAMLRKHGEQQLPAVGLTNHQLFVGVFAQWCSVRTPRESSHGLVTDPHSARF 778

DB 683 AYYAAQKWVRKRGPEHPRLRLKTYTNQJFPIAQNWCIKRSQSITYQLVLTDKAPERY 742  
 QY 779 RVLGTLNSNRDILRRPGCVSPNPGOLCEW 811  
 DB 743 RVLGVSQPEEGRGFHCPKSPMNVHKSVM 775

## RESULT 8

ECBL\_MOUSE  
 ID ECBL\_MOUSE STANDARD; PRT; 775 AA.  
 AC Q9JMT0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein)  
 GN (Damage-induced neuronal endopeptidase).  
 OS ECBL OR XCE OR DINE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20226106; PubMed=10759559;  
 RA KIRYU-Seo S., Sasaki M., Yokohama H., Nakagomi S., Hirayama T.,  
 Aoki S., Wada K., Kiyama H.;  
 RT "Damage-induced neuronal endopeptidase (DINE) is a unique  
 RT metalloprotease expressed in response to neuronal damage and  
 RT activates superoxide scavengers";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4345-4350(2000).  
 CC -1- FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC -1- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; AB026294; BAA95005.1; -.  
 CC DR HSSP; P08473; IDMT.  
 CC DR MEROPS; M13.007; -.  
 CC DR MGD; MGI:1343461; Ecbl1.  
 CC GO; GO:0004222; F:metalloendopeptidase activity; IDA.  
 CC DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 CC DR InterPro; IPR000718; Peptidase\_M13.  
 CC DR InterPro; IPR008753; Peptidase\_M13\_N.  
 CC DR Pfam; PF01431; Peptidase\_M13; 1.  
 CC DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 CC DR PRINTS; PR00786; NEPRILYSIN.  
 CC DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 CC KM Hydrolyase; Protease; Metalloprotease; Metal-binding; Zinc;  
 CC KW Glycoprotein; Transmembrane; Signal-anchor.  
 CC FT DOMAIN 1 61  
 CC FT TRANSMEM 62 82  
 CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 CC FT (POTENTIAL).  
 CC FT LUMENAL (POTENTIAL).  
 CC FT ZINC (CATALYTIC) (BY SIMILARITY).  
 CC FT ACT\_SITE 612 612  
 CC FT METAL 613 613  
 CC FT METAL 616 616  
 CC FT METAL 672 672  
 CC FT CARBOHYD 255 255  
 CC FT CARBOHYD 322 322  
 CC FT CARBOHYD 656 656  
 CC FT SEQUENCE 775 AA; 87993 MW; 53A4595D7C5F34B9 CRC64;



Query Match 32.6%; Score 1395.5; DB 1; Length 775;  
 Best Local Similarity 36.4%; Pred. No. 8.3e-86;  
 Matches 296; Conservative 156; Mismatches 292; Indels 69; Gaps 15;

QY EFTVEGASDANAEVGGASPSFGSPG--MTPGPSSGSLTWRVYCPHLRSISG----82  
 DB 2 EAFVSMTHAYDEFOEVKTVSRCTGGARGGSLPPGFRSG-----KSAAGSRG 51  
 QY 83 -----LCRTWVFGKGTROLLGSRTOLEVLGASILLALLGLVALGVYHRD 134  
 DB 52 LPRMNRREVLLGLVPAALCAIILAMLLKYLGPDAAGGAGCGCG-----100  
 QY 135 PSSTCTCTACTACVAGKILESIDRGVSPCEDFIOFGCGGMITRRNPLPDGSRMNTNSLW 194  
 DB 101 PER-----KAFAPAAAFSLANLASSIDPCODFYFAGGWMRRRAIPDDLTGTGTAALIG 155  
 QY 195 DONOALIKHLLENTTFNNSSEABOKTORFLTSLQVRIEELAGOPRLDIKIGGNIT 254  
 DB 156 EQNEERLRRLARPTGGPGGAQKVAFRSCIDMKEIRLGRPMLEVIDGCGDLG 215  
 QY 255 GP-----WDONFMEVLKAVAGTYRATPFTVYISADSKSSNVIOVDSGLFLPS 306  
 DB 216 GAADREPAARWDLN---RLYKAGGVYSAALFSLTSLDRSSRYVIRIDDGDLTPE 272  
 QY 307 RDIYLLAR-TANEXLTAIYLDYMEELGMLGCRPTSTREQVQLLEIQLANTVPO--D 363  
 DB 273 RTIYLAQDESEKILAAVRFVMOGLRLTGA--DAVEOKAOEILQLEORLANTSVSEYD 330  
 QY 364 QRRDEEKIYHKMSISELOALPAMDLEFSLPLSPL---ELSDSEPVVYGMDDYQOVS 420  
 DB 331 LRNDVSSANKVVLGQLQKIIPHLOW---KMLLDQIFQEDPSEEBEVLLADYMQOVS 366  
 QY 421 ELINRTERPSILNNVYLINVLQKTTSLDRRFSASOERLLETLYGTXKSCVPR--WOTCIS 478  
 DB 387 QLRSTPRIRLTHVYLVKRVVVLSEHLSPFREALHELAKEMGNDK--POELARVCLG 443  
 QY 479 NTDDALGALGSLFYKATPDRSGEITABGMISEKRTAFEEALGQLVMDKTOQAAXKA 538  
 DB 444 QARRHFEMALGALFVHEHFAASAKAQOVLVEDIKYLLQRLBELMDMDAQOTAAAPAKL 503  
 QY 539 DAYIDMIGFPDLEPERLEDDVYDGYEISDSFQONMLNTYNFSAKYAMADLRKRPBRDQ 598  
 DB 504 QYMMWVGDFELFKPAVDKEYE-FVHEKTYFKILNIRSISQLSYKIKIQEVDKST 562  
 QY 599 WSNTPQTVANAYYLPTKNEIYFPAGIIOAPFYARNHPALNFGGIGVNGHELTAPDDOG 658  
 DB 563 WLPRLQNLNAYLIPNKQMYVPAIGIPLTYDPPQSLNAYGIGITIGHELTGVDWG 622  
 QY 659 REYDKEGNLPAPWONESLAPRNHTACMEQOYNQYNGERLNGRQTLGENIADNGLKA 718  
 DB 623 GQYDRSGNLLHMTWTEASYSRFLHAEICIVLYDNFTYVYNGRVNGKTLGENDMGGLKL 682  
 QY 719 ANAYAKMLRKGEBOQLPAVGLTNHQLFVFGFQAVNCSVRTESSHEGLVDPHSPARF 778  
 DB 683 AYTAAYQWVKEHGEPEHLKLTHTNOLFFIAPRQWMCIRKRSQSYLYQVLTDKHAPHY 742  
 QY 779 RVIGTILNSRDPLRHFGCPVSPMNPQOLCEW 811  
 DB 743 RVLGSVSGPEEFGAFHCPKDSPMNPVHKCSVM 775

RESULT 9  
 ECEL\_HUMAN STANDARD; PRT; 775 AA.  
 AC 095672; Q9N95; (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Endothelin-converting enzyme-like 1 (EC 3.4.24.-) (Xce protein).  
 GN ECEL1 OR XCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Caudate, and Spinal cord;  
 RX MEDLINE=9913287; PubMed=9911490;  
 RA Valdenaire O., Richards J.G., Paul R.L.M., Schweizer A.;  
 RT "XCE", a new member of the endothelin-converting enzyme and neutral  
 RT endopeptidase family, is preferentially expressed in the CNS.";  
 RL Brain Res. Mol. Brain Res. 64:211-221(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20164043; PubMed=10698686;  
 RA Valdenaire O., Rohrbacher E., Langeveld A., Schweizer A., Meijers C.;  
 RT "Organization and chromosomal localization of the human ECEL1 (XCE)  
 RT gene encoding a zinc metalloproteinase involved in the nervous control  
 RT of respiration.";  
 RL Biochem. J. 346:611-616(2000).  
 CC - FUNCTION: May contribute to the degradation of peptide hormones  
 CC and be involved in the inactivation of neuronal peptides.  
 CC - COFACTOR: Binds 1 zinc ion (By similarity).  
 CC - SUBCELLULAR LOCATION: Type II membrane protein (By similarity).  
 CC - TISSUE SPECIFICITY: Highly expressed in the CNS, in particular in  
 CC putamen, spinal cord, medulla and subthalamic nucleus. A strong  
 CC signal was also detected in uterine subepithelial cells and around  
 CC renal blood vessels. Detected at lower levels in amygdala,  
 CC caudate, thalamus, pancreas and skeletal muscle. Detected at very  
 CC low levels in substantia nigra, cerebellum, cortex, corpus  
 CC callosum and hippocampus.  
 CC - PFM: N-glycosylated.  
 CC - SIMILARITY: Belongs to peptidase family M13.  
 CC  
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 CC  
 CC EMBL: Y16187; CAA7613.1; -  
 CC EMBL: AJ130734; CAB86601.1; -  
 CC HSSP: P08473; IDMT.  
 CC MEROPS: M13.007; -  
 CC GeneW: HGNC:3147; ECEL1.  
 DR MIM: 605896; -  
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO: GO:0008237; F: metalloproteinase activity; TAS.  
 DR GO: GO:0007218; P: neuro-peptide signaling pathway; TAS.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro: IPR00718; Peptidase\_M13.  
 DR InterPro: IPR008753; Peptidase\_M13\_N.  
 DR Pfam: PF01431; Peptidase\_M13\_1.  
 DR Pfam: PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS: PR00786; NEPRILYSIN.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR HydroLase: Protease; Metalloprotease; Metal-binding; Zinc;  
 KW Glycoprotein; Signal-anchor; Polymorphism.  
 KW Cytoplasmic (POTENTIAL).  
 KW SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT TRANSMEM 60 82  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 82  
 FT  
 FT DOMAIN 83 775  
 FT METAL 612 612  
 FT ACT\_SITE 613 613  
 FT METAL 616 616  
 FT METAL 672 672  
 FT CARBOHYD 255 255  
 FT CARBOHYD 322 322  
 FT CARBOHYD 656 656  
 FT VARIANT 10 10  
 FT  
 FT VARIANT 328 328  
 FT  
 FT CONFLICT 286 286  
 V -> I (1N REF. 2).  
 /FTID=VAR 012813.  
 Y -> H (1N dBSNP:1529874).  
 /FTID=VAR 012814.





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CC	or send an email to licenses@isb.sib.ch).					
CC	-----					
DR	EMBL,	X07166;	CAA30157.1;	ALT_INIT.		
DR	EMBL,	Y00811;	CAAG8752.1;	-		
DR	EMBL,	J03779;	AAA51915.1;	-		
DR	EMBL,	M26628;	AAA52294.1;	-		
DR	EMBL,	M26607;	AAA52294.1;	JOINED.		
DR	EMBL,	M26608;	AAA52294.1;	JOINED.		
DR	EMBL,	M26609;	AAA52294.1;	JOINED.		
DR	EMBL,	M26610;	AAA52294.1;	JOINED.		
DR	EMBL,	M26611;	AAA52294.1;	JOINED.		
DR	EMBL,	M26612;	AAA52294.1;	JOINED.		
DR	EMBL,	M26613;	AAA52294.1;	JOINED.		
DR	EMBL,	M26614;	AAA52294.1;	JOINED.		
DR	EMBL,	M26615;	AAA52294.1;	JOINED.		
DR	EMBL,	M26616;	AAA52294.1;	JOINED.		
DR	EMBL,	M26617;	AAA52294.1;	JOINED.		
DR	EMBL,	M26618;	AAA52294.1;	JOINED.		
DR	EMBL,	M26619;	AAA52294.1;	JOINED.		
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DR	EMBL,	M26621;	AAA52294.1;	JOINED.		
DR	EMBL,	M26622;	AAA52294.1;	JOINED.		
DR	EMBL,	M26623;	AAA52294.1;	JOINED.		
DR	EMBL,	M26624;	AAA52294.1;	JOINED.		
DR	EMBL,	M26625;	AAA52294.1;	JOINED.		
DR	EMBL,	M26626;	AAA52294.1;	JOINED.		
DR	EMBL,	M26627;	AAA52294.1;	JOINED.		
DR	PIR,	A41387;	HYHUN.			
DR	PDB,	1DMT;	20-DEC-00.			
DR	PDB,	1DL9;	13-DEC-00.			
DR	MEROPE;	M13_001;	-;			
DR	GeneW;	HGNC:	7154;	NME.		
DR	MIM;	120520;	-;			
DR	GO:	GO:0005887;	C:integral to plasma membrane; TAS.			
DR	GO:	GO:0008237;	F:metallopeptidase activity; TAS.			
DR	GO:	GO:0007267;	P:cell-cell signaling; TAS.			
DR	GO:	GO:0006508;	P:proteolysis and peptidolysis; TAS.			
DR	InterPro;	IPIR006025;	Pept_M_Zn_BS.			
DR	InterPro;	IPIR000718;	Peptidase_M13_N.			
DR	InterPro;	IPIR008753;	Peptidase_M13_N.			
DR	pfam;	PF01431;	Peptidase_M13_I.			
DR	PRINTS;	PR05649;	Peptidase_M13_N_1.			
DR	PRINTS;	PRO0786;	NEPRILYSIN.			
DR	PROSITE;	PS00142;	ZINC_PROTEASE; 1.			
KM	Hydrolase;	Metalloprotease;	Metal-binding; zinc; Transmembrane;			
KM	Glycoprotein;	Signal-anchor;	3D-structure.			
FT	INIT_MET	0	0			
FT	DOMAIN	1	27			
FT	TRANSMEM	28	50			
FT	DOMAIN	51	749			
FT	DOMAIN	15	22			
FT	BINDING	102	102			
FT	METAL	583	583			
FT	METAL	587	587			
FT	ACT SITE	590	590			
FT	METAL	646	646			
FT	ACT SITE	650	650			
FT	DISULFID	56	61			
FT	DISULFID	79	734			
FT	DISULFID	87	694			
FT	DISULFID	142	410			
FT	DISULFID	233	241			
FT	DISULFID	620	746			
FT	CARBOHYD	144	144			
FT	CARBOHYD	284	284			
FT	CARBOHYD	324	324			
FT	CARBOHYD	627	627			
FT	CONFLICT	25	25			
FT	CONFLICT	43	43			
FT	CONFLICT	80	80			
FT	CONFLICT	303	303			

	FT	STRAND	55	55
FT	HELI	HELI	59	71
FT	TURN	TURN	74	75
FT	TURN	TURN	78	80
FT	HELI	HELI	82	93
FT	TURN	TURN	98	99
FT	STRAND	STRAND	102	104
FT	HELI	HELI	105	121
FT	TURN	TURN	126	127
FT	HELI	HELI	130	143
FT	HELI	HELI	145	150
FT	TURN	TURN	151	153
FT	HELI	HELI	154	159
FT	HELI	HELI	160	163
FT	TURN	TURN	164	164
FT	HELI	HELI	167	169
FT	TURN	TURN	171	172
FT	HELI	HELI	173	176
FT	TURN	TURN	177	180
FT	HELI	HELI	183	194
FT	STRAND	STRAND	201	207
FT	TURN	TURN	208	209
FT	HELI	HELI	210	219
FT	STRAND	STRAND	228	232
FT	HELI	HELI	235	237
FT	HELI	HELI	238	258
FT	TURN	TURN	259	260
FT	HELI	HELI	265	285
FT	HELI	HELI	289	291
FT	HELI	HELI	295	298
FT	STRAND	STRAND	301	303
FT	HELI	HELI	304	310
FT	TURN	TURN	316	317
FT	HELI	HELI	322	330
FT	HELI	HELI	331	333
FT	TURN	TURN	334	334
FT	TURN	TURN	339	340
FT	STRAND	STRAND	342	345
FT	HELI	HELI	348	358
FT	TURN	TURN	359	360
FT	HELI	HELI	363	378

Query Match 30.0%; Score 1282.5; DB 1; Length 749;  
 Best Local Similarity 36.0%; Pred. No. 3.1e-78;  
 Matches 264; Conservative 149; Mismatches 289; Indels 31; Gaps 13

QY	103	TQLEVLNAGASLLLAALLGLCLVNLGVQYHNDPSHSTGLTEACIRVAGKIIESTLDRGVS	162
DB	24	TPLEISLSVLVLLTLITIAV-TWIALYATY---DDGICKSSDCKISAAKLQNMADATPE	78
QY	163	CEDFYQFSCGGMIRRNPLPDGRSRWNTFNSLMDQALIKHLLENTTFNNSSEAEQKTC	222
DB	79	CTDFPKYACGGMLKRNVIPEFTSSRYGNPDILRDELEVVLKVLQVLEPK-TEDIVAVQKKA	137
QY	223	FYLSCLQVERIEELGAQPLRLDLEIKIGGMNI-TGEMDQ-DNFEVLKAVA--GTYPAT	276
DB	138	LYRSCINSAIDSRGEBPLKLPLDIYGMVATENMEQKYGASWAEKAIQAQNSKYGK	197
QY	277	PEFYIYISADSKSNSNVIOVDQGLPLPSRDYIYLRANKEVYLTAIYDYMELGMLGG	336
DB	198	VLINLPEVTDKNSNVNVIHIDQPLGLPSRDYECTGIYKACTAYVDPMISVARLIRQ	257
QY	337	R---PTSRRE---QMOQVLELEIOLANTTVPODGRDEKTIYHKMSISLQ-----ALA	384
DB	258	EERPIDENQALALEMKYMELEKEIYANATAPEDBRNDPMLLYNKTTIAQIQNPSLEING	317
QY	385	PSMDWLEFLSLSPLELS--DSEPVVVYGMVDYLAQVSELINRTEPSILANNYLINLVQK	442
DB	318	KPFWMLNFTNIMSTVNISITNEEDVVVYADEVILTKLPILTKYSARDLQNLMSWRFLMD	377
QY	443	TTSSLIDRRFEBAQEKLETLTYGTSKSCVPKQTCISNTDDALGPAIGSLFYKATFDROSK	502
DB	378	LVSSLISRYKYSKSRNAFRALVGT-TSETATYRRCANVYNGMEANVGBLYVEAARAGBSK	436



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QY 277 PFFTVYISADSKSSNSVIVQDQSGFLPFRSDYILNRTANEKVLTAVDYMEELGMLT-- 334
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 198 VLINFEVGDGDKNSNNHIIHIDQPLGLPGRVYECTGIVKACATAYVDFMLAVAKLIRQ 257
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 335 -GGPFTSTRE---QMOQVLELEIQLANITVPDQDRDEEKIYKXISISELQ-----ALA 384
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 258 BEGLPIDEQIISVENMKVMELEKEIATNATTKSEDRDPMLLYNKMTLQIQNNFSLIEING 317
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 365 PSMDELFLISFLSLPLELS--DSEPVYVYGMVYLOQVSLINKRTESILANTLYINLVOK 442
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 318 KPFSNPNFNEIMSTVNINIPNEEDVYVAPPEYLKIKELIKYEPFRDQNLPSMRFIMD 377
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 443 TTSSDRPPESAQOEKLETLTGKTSCEVPMQTCISNTDLAGFALGSLFVATPDRQSK 502
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 378 LVSSLSRYTKSRNAPFKALYGTTSESA-TWRCANYNNGNENNAVGRVYDAAPAGEBK 436
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 503 EIAEGMISEIRTAFEALGOLVWMDKTRQAARADAIYDMIGPDPFIL-EPKELDLYV 561
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 437 HVEDLLIAQIREVFLOTLDLITWMDAETKKAEKALAIKERIGVDDIVSNDKNLNEY 496
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 562 DGEVISEDSFPMNMLNLYPSAKWADQARKPSRDQMSMTQTVNAYLYLPTKNEIVPFA 621
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 497 LELNKEDEYFENIIQNLKFSQSKQKREKVDDEWITGAAYVAFSSGRNOIVPFA 556
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 622 GILQAPFYARNHPKALNFGIGVYMGHELTTHAFDDQGREYDEKGNLRPMQNESLAAPRN 681
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 557 GILQPPFSAQOQNSNLNIGSIGMIVGHEITTHGFDDNGRFRNKGDLVDMWTQOASANNFE 616
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 682 HTACMEBOYNOYO---VNGERLNGRQTLGENTADNGLKAAYNAKAMLRKHGEEOQLPA 738
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 617 OSQGVVYQGNFSWDLAQGLHNGINTLIGENTADNGIGQAVRAYQNYVKKNGEELKPLFG 676
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 739 VGLTHQLPFVGFQAVQVGVTRPSSHEGLVTDHPSPAFRVLGLTSLNSKRDILRHFGCV 798
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 677 IDLNHKQLEFNLPAWVCGTYRPEYAVNSIKTDVHSPGNFRILIGSLQNSVSESEAFQCPK 736
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 799 GSPMNPOLCEVW 811
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 737 NSYNMPEKKCKRW 749
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
NEP_RAT
ID NEP_RAT STANDARD; PRT; 749 AA.
AC POT861;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NEP)
DB (Enkephalinase).
GN MME.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxId=10116;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87213218; PubMed=3555489;
RA Malfroy B., Schofield P.R., Kuang W.-J., Seeburg P.H., Mason A.J.,
RA Henzel W.J.;
RT "Molecular cloning and amino acid sequence of rat enkephalinase.";
RL Biochem. Biophys. Res. Commun. 144:59-66(1987).
RN [2]
ACTIVE SITE ARG-102.
RP MEDLINE=89197908; PubMed=2703483;
RX Bateman R.C. Jr., Jackson D., Slaughter C.A., Unithan S., Chai Y.G.,
RA Moonaw C., Hersh L.B.;
RT "Identification of the active-site arginine in rat neutral
endopeptidase 24.11 (enkephalinase) as arginine 102 and analysis of a
glutamine 102 mutant.";
RL J. Biol. Chem. 264:6151-6157(1989).
CC -1- FUNCTION: Thermoalysin-like specificity, but is almost confined on
acting on polypeptides of up to 30 amino acids. Biologically

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CC important in the destruction of opioid peptides such as Met- and
CC Leu-enkephalins by cleavage of a Gly-Phe bond.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage at the amino group of
CC hydrophobic residues in insulin, casein, hemoglobin, and a number
CC of other proteins and polypeptides.
CC -1- COFACTOR: Binds 1 zinc ion per subunit.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: Belongs to peptidase family M13.
CC -----
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CC -----
CC EMBL, M15944; AAA41116.1; -.
CC DR PIR, A29295; HYRTN.
CC DR HSSP, P08473; 1DMT.
CC DR MEROPS, M13.001; -.
CC DR InterPro, IPR006025; Pept_M_Zn_BS.
CC DR InterPro, IPR000718; Peptidase_M13.
CC DR InterPro, IPR008753; Peptidase_M13_N.
CC DR Pfam, PF01431; Peptidase_M13_1.
CC DR Pfam, PF05649; Peptidase_M13_N_1.
CC DR PRINTS, PR00786; NEPRILYSIN.
CC DR PROSITE, PS00142; ZINC_PROTEASE, 1.
CC DR HydroLase; Metalloprotease; Metal-binding; Zinc; Transmembrane;
CC KW Glycoprotein; Signal-anchor.
CC FT INIT MET 0
CC FT DOMAIN 1 27
CC FT TRANSMEM 28 50
CC FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 51 749
CC FT BINDING 15 22
CC FT BINDING 102 102
CC FT METAL 583 583
CC FT ACT SITE 584 584
CC FT METAL 587 587
CC FT METAL 646 646
CC FT ACT SITE 650 650
CC FT ACT SITE 56 61
CC FT DISULFID 79 734
CC FT DISULFID 87 694
CC FT DISULFID 142 410
CC FT DISULFID 233 241
CC FT DISULFID 620 746
CC FT CARBOHYD 144 144
CC FT CARBOHYD 210 210
CC FT CARBOHYD 284 284
CC FT CARBOHYD 310 310
CC FT CARBOHYD 324 324
CC FT CARBOHYD 627 627
CC FT CARBOHYD 627 627
CC FT SEQUENCE 749 AA; 85663 MW; 89B0EC50A9016A47 CRC64;
CC -----
CC Query Match 29.7%; Score 1272.5; DB 1; Length 749;
CC Best Local Similarity 35.6%; Pred. No. 1.4e-77;
CC Matches 261; Conservative 148; Mismatches 293; Indels 31; Gaps 13;
QY 103 TQLEVLVLAGSLAALLGLGVALVGYQHPDPSHSTLCTACRIVACKILESLRGVSP 162
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 24 TPLEISLVVLLTITIV-TWIALYATY---DDGICKSDGCTISAKRLIQNMDSAP 78
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 163 CEDFYQSCGGMIRNPLPDRSRNWTNFSIMDQOALIKHLIENTTNSSEADQKQR 222
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 79 CTDPEFYKACGWLKRNVIPTSSRSYNSFDLRDELVLITKOVLTQEPK-TEDIVAQKAKT 137
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 223 FYLSLQVRIERBELGAQPLRDLIERIGVGNITGP-WDQ-DNFEVLKAVA---GTYYAT 276
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 138 LYRSCINSAISDSRGQPLRLTLPDIYGPWPAASQWMEQYGTSTWAEKSIQNLNSKYGKK 197
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 277 PFFTVYISADSKSSNSVIVQDQSGFLPFRSDYILNRTANEKVLTAVDYMEELGMLTGG 336

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Db      198  VLINEFVGTTDDKNSHTGHIHFDPRLGRLPSRDYECTGYTKAATAVDFMISVARLKRQ 257
      337  R---PTSTR---OMQOVLELEIOLANITVPDORREDEKIKHKSISELQ-----ALA 384
      258  BGRRLPIDENQQLBENMKWLEKEIANATTKBEDRNDPMLLVNKTMLATLQNNPSELENG 317
Qy      385  PSMDWLEPLSLSP--LELSDEPVYVGMDOVLQOVSLEINRTEPSLIANTYLINLVOK 442
      318  KPFSWSNPFNEIMSTVINIIONEBEVVVYAPBYLTCLKPLTKYSPRDLQNLMSRPFIND 377
Qy      443  TTSSLDREPRESAOEKLETLTYGKKSCVBRMOTCSNTDLAGPALGSLFKVATPDPGK 502
      378  LVSSLSRNTKESNNAFRKALYGI-TSEIATWRCAVYVGNENNAVGRLYVEAPAGSEK 436
Qy      503  EIAEGMISIRTAFEELGOLVWDEKTRQAAKEKADAIYDIGPPFLL-EPKELDDVY 561
      437  HVVEDLIAQIREVFIOTLDDLTMMDAFETKKAEKALAIKERIGYDDIISMENTLNNEY 496
Db      562  DGEYISEDSFPQNMMLNYPNPAKWMADQLRKPPSRDQMSMTPTQTVNAYTLPKNEIVPA 621
      497  LELNKEEYEFENIIIONLFKFSQSKOLKREKVDKDEWISGAVVNAFVSSGNQIVPFA 556
Qy      622  GILQAPFYARNHPKALNPGSIGVVMGHELTTHAFDDQREYDKGNRPWQNESLAAPRN 681
      557  GILQPPFPARQSNLSINYGIGVIGHEITHGDDGNRNPNQDGLVDMWTOOSANNFQD 616
Qy      682  HTACMEEQNOYO--VNGERLNGRQTLGENTADNGLAAVNAVYKAMLRKGEEOQLPA 738
      617  QGQCMVYQGNFTWDLAAGHNGITLTGENTADNGIGQARAYQNVYKXNGEELPLPG 676
Qy      739  VGLTTHQLFFVGAQVQCVTRPESHEGLVTDPHSPARFVLGTSNRDPLRHFGCV 798
      677  LDLNKHQLPFLIPAQVCGTYRPEVAVNSIKTDVHSPGNFRITGLQNSAEFADAFHCRK 736
Qy      799  GSPNPNQGLCEVY 811
      737  NSYNPDKCRVW 749
Db
Qy      799  GSPNPNQGLCEVY 811
      737  NSYNPDKCRVW 749
Db

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RESULT 14  
PEX\_HUMAN STANDARD PRT: 749 AA.  
AC P78562; 000678; Q13646; Q93032; Q93827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phosphate regulating neutral endopeptidase (EC 3.4.24.-)  
DE (Metalloendopeptidase homolog PEX) (X-linked hypophosphatemia protein)  
DE (HYP) (Vitamin D-resistant hypophosphatemic rickets protein).  
GN PHEX OR PEX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND VARIANTS HYP ARG-85; LEU-534; ARG-579 AND PRO-651.  
RX MEDLINE=97343325; PubMed=9199930;  
RA Brandau F., Strom T.M., Hennig S., Boeddrich A., Lorenz B., Borzym K., Pohl T., Oudet C.L., Cagnoli M., Steffens C., Klages S., Weitinger T., Lehrach H.;  
RT "Genomic organization of the human PEX gene mutated in X-linked dominant hypophosphatemic rickets.";  
RL genome Res. 7:573-585(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97332252; PubMed=9077527;  
RA Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauchier C., Goodyer C.G., Tenenhouse H.S.;  
RT "Pex/PEX tissue distribution and evidence for a deletion in the 3' region of the Pex gene in X-linked hypophosphatemic mice.";

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RL      J. Clin. Invest. 99:1200-1209(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone;
RX MEDLINE=97343443; PubMed=9199999;
RA Guo R., Quarles L.D.;
RT "Cloning and sequencing of human PEX from a bone cDNA library: evidence for its developmental stage-specific regulation in osteoblasts.";
RL J. Bone Miner. Res. 12:1009-1017(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Lipman M.L., Panda D., Henderson J.E., Shen Y., Goltzman D., Karpelis A.C.;
RX Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224400; PubMed=9070661;
RA Grieff M., Mumm S., Waelitz P., Mazzarella R., Whyte M.P., Thakker R.V., Schiessinger D.;
RT "Expression and cloning of the human X-linked hypophosphatemia gene cDNA.";
RL Biochem. Biophys. Res. Commun. 231:635-639(1997).
RN [6]
RP SEQUENCE OF 4-641 FROM N.A.
RX MEDLINE=96024647; PubMed=7550339;
RA Francis F., Hennig S., Korn B., Reinhardt R., de Jong P., Pouscka A., Lehrach H., Rowe P.S.N., Goulding J.N., Sumnerfield T., Mountford R., Read A.P., Popowska E., Pronicka K., Davies K.B., Orlordan J.L.H., Haneur A., Strom T.M., Dreznar M.K., Oudet C.L., Pannetier S., Mohrner K.L., Murken J., Weitinger T.;
RT "A gene (PEX) with homologies to endopeptidases is mutated in patients with X-linked hypophosphatemic rickets. The HYP Consortium.";
RL Nat. Genet. 11:130-136(1995).
RN [7]
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP VARIANTS HYP TYR-85; CYS-166; SER-252; ILE-253 AND VAL-579.
RX MEDLINE=97260404; PubMed=9106524;
RA Holm I.A., Huang X., Kunkel L.M.;
RT "Mutational analysis of the PEX gene in patients with X-linked hypophosphatemic rickets.";
RL Am. J. Hum. Genet. 60:790-797(1997).
RN [9]
RP VARIANTS HYP SER-77; PRO-138; LEU-534 AND ARG-579.
RX MEDLINE=9725287; PubMed=9097956;
RA Rowe P.S.N., Oudet C.L., Francis F., Sinding C., Pannetier S., Econs M.J., Strom T.M., Weitinger T., Garabedian M., David A., Machner M.-A., Questiaux E., Popowska E., Pronicka K., Read A.P., Mokrzycki A., Glorieux F.H., Dreznar M.K., Haneur A., Lehrach H., Goulding J.N., Orlordan J.L.H.;
RT "Distribution of mutations in the PEX gene in families with X-linked hypophosphatemic rickets (HYP)."
RL Hum. Mol. Genet. 6:539-549(1997).
RN [10]
RP VARIANT HYP PRO-555.
RX MEDLINE=96439582; PubMed=9768646;
RA Econs M.J., Friedman N.B., Rowe P.S.N., Speer M.C., Francis F., Strom T.M., Oudet C.L., Smith J.A., Nimmiya V.T., Lee B.B., Bergen H.;
RT "A PEX gene mutation is responsible for adult-onset vitamin D-resistant hypophosphatemic osteomalacia: evidence that the disorder is not a distinct entity from X-linked hypophosphatemic rickets.";
RL J. Clin. Endocrinol. Metab. 83:3459-3462(1998).
RN [11]
RP VARIANTS HYP PHE-317; LEU-534; ARG-579; ARG-621; ASN-680 DEL; THR-720; TYR-731 AND ARG-749.
RX MEDLINE=98439610; PubMed=9768674;
RA Dixon P.H., Christie P.T., Wooding C., Trump D., Grieff M., Holm I.A.,

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RA Gertner J.M., Schmidtke J., Shah B., Shaw N., Smith C., Tau C.,  
RA Schlesinger D., Whyte M.P., Thakker R.V.;  
RT "Mutational analysis of PHEX gene in X-linked hypophosphatemia.";  
RL J. Clin. Endocrinol. Metab. 83:3615-3623(1998).  
[12]  
RA VARIANTS HYP SER-80; PHE-142; GLY-237; CYS-530; ASP-573; SER-733 AND  
RP TRP-746.  
RX MEDLINE=99368844; PubMed=10439971;  
RA Filisetti D., Oestermann G., von Bredow M., Strom T.M., Filler G.,  
RA Ethich J., Panetier S., Garnier J.-M., Rowe P.S.N., Francis F.,  
RA Juliette A., Hanauer A., Econe M.J., Oudet C.L.;  
RT "Non-random distribution of mutations in the PHEX gene, and  
RT under-detected missense mutations at non-conserved residues.";  
RL Eur. J. Hum. Genet. 7:615-619(1999).  
[13]  
RX VARIANTS HYP PHE-85; PRO-141; VAL-341 DEL; PRO-567; LYS-680 AND  
RP TYR-693.  
RX MEDLINE=20202840; PubMed=10737991;  
RA Tyynismaa H., Kaitila I., Naentoe-Salonen K., Ala-Houhala M.,  
RA Alitalo T.;  
RT "Identification of fifteen novel PHEX gene mutations in Finnish  
RT patients with hypophosphatemic rickets.";  
RL Hum. Mutat. 15:383-384(2000).  
[14]  
RX VARIANTS HYP ARG-160 AND ASN-444 INS.  
RX MEDLINE=20461419; PubMed=11004247;  
RA Sato K., Tajima T., Nakae J., Adachi M., Asakura Y., Tachibana K.,  
RA Suwa S., Katsumata N., Tanaka T., Hayashi Y., Abe S., Mutsaers M.,  
RA Okhara K., Shinozaki N., Fujieda K.;  
RT "Three novel PHEX gene mutations in Japanese patients with X-linked  
RT hypophosphatemic rickets.";  
RL Pediatr. Res. 48:536-540(2000).  
CC -1- FUNCTION: Probably involved in bone and dentin mineralization  
CC and renal phosphate reabsorption.  
CC -1- COPACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: Lymphocyte and fetal brain; not in adult  
CC brain, placenta, skeletal muscle and pancreas; not in adult and  
CC fetal heart, lung, liver and kidney.  
CC -1- DISEASE: Defects in PHEX are a cause of X-linked hypophosphatemic  
CC rickets (HYP) [MIM:307800]. HYP is an X-linked dominant disorder  
CC characterized by impaired phosphate uptake in the kidney, which is  
CC likely to be caused by abnormal regulation of sodium phosphate  
CC cotransport in the proximal tubules. Clinical manifestations  
CC include skeletal deformities, growth failure, craniosynostosis,  
CC extramedullary calcifications, pseudofractures in lower  
CC extremities, and muscular hypotonia with onset in early childhood.  
CC X-linked hypophosphatemic rickets is the most common form of  
CC hypophosphatemia with an incidence of 1 in 20000.  
CC -1- SIMILARITY: Belongs to peptidase family M13.  
CC -1- DATABASE: NAME=PHEXdb; WWW="http://data.mcgill.ca/phexdb/".  
CC -----  
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CC -----  
DR EMBL; Y10196; CAA71258.1; -;  
DR EMBL; U75645; AAB47749.1; -;  
DR EMBL; U82970; AAC24487.1; -;  
DR EMBL; U87284; AAB47562.1; -;  
DR EMBL; Y08111; CAA69326.1; -;  
DR EMBL; Y08112; CAA69326.1; JOINED.  
DR EMBL; Y08113; CAA69326.1; JOINED.  
DR EMBL; Y08114; CAA69326.1; JOINED.  
DR EMBL; Y08115; CAA69326.1; JOINED.  
DR EMBL; Y08116; CAA69326.1; JOINED.  
DR EMBL; Y08117; CAA69326.1; JOINED.  
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DR EMBL; Y08508; CAA69326.1; JOINED.  
DR EMBL; Y08509; CAA69326.1; JOINED.  
DR EMBL; Y08510; CAA69326.1; JOINED.  
DR EMBL; Y08511; CAA69326.1; JOINED.  
DR EMBL; Y08512; CAA69326.1; JOINED.  
DR EMBL; Y08513; CAA69326.1; JOINED

Db 664 RROGLEBLLPGRITFTNNQFLPFLSYAHVCNSYREARBEQVIGASHPPORVNGAISN 723  
 Qy 787 SRDFLRHFGCPVGPSPMPC-QUCEWV 811  
 Db 724 REEFKAFRCPPNSITMRGMSCRIM 749

RESULT 15  
 PEX\_MOUSE STANDARD; PRT; 749 AA.  
 ID PEX\_MOUSE  
 AC P70669; P97439; (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Metalloendopeptidase homolog PEX (EC 3.4.24.-) (Phosphate regulating neutral endopeptidase) (X-linked hypophosphatemia protein) (HYP)  
 DE (Vitamin D-resistant hypophosphatemic rickets protein).  
 GN PHEX OR PEX OR HYP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96411643; PubMed=8812412;  
 RA Du L., Desbarats M., Viel J., Glorieux F.H., Cawthoim C., Escarot B.;  
 RT "cDNA cloning of the murine Pex gene implicated in X-linked hypophosphatemia and evidence for expression in bone.";  
 RL Genomics 36:22-28(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97217775; PubMed=9063736;  
 RA Strom T.M., Francis F., Lorenz B., Boeddrich A., Econs M.J.,  
 RA Lehnach H., Meitinger T.;  
 RT "Pex gene deletions in Cy and Hyp mice provide mouse models for X-linked hypophosphatemia.";  
 RL Hum. Mol. Genet. 6:165-171(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=97232252; PubMed=9077527;  
 RA Beck L., Soumounou Y., Martel J., Krishnamurthy G., Gauthier C.,  
 RA Goodover C.G., Tenenhouse H.S.;  
 RT "Pex/pex tissue distribution and evidence for a deletion in the 3' region of the Pex gene in X-linked hypophosphatemic mice.";  
 RL J. Clin. Invest. 99:1200-1209(1997).  
 CC -1- FUNCTION: Probably involved in bone and dentin mineralization and renal phosphate reabsorption.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Bone.  
 CC -1- SIMILARITY: Belongs to peptidase family M13.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).  
 CC  
 CC EMBL; U49908; AAC6502.1; -  
 DR EMBL; U73910; AAC25962.1; -  
 DR EMBL; U73912; AAC25964.1; -  
 DR EMBL; U73913; AAC25965.1; -  
 DR EMBL; U73914; AAC25966.1; -  
 DR EMBL; U73911; AAC25963.1; -  
 DR EMBL; U73915; AAC25967.1; -  
 DR EMBL; U75646; AAB47750.1; -  
 DR HSSP; P08473; IDMT.  
 DR MEROPS: M13.091; -  
 DR MGD; MGI:107489; PheX.

DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR Pfam; PF01431; Peptidase\_M13\_1.  
 DR Pfam; PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR Biomineralization; Hydrolase; Metalloprotease; Zinc; Signal-anchor;  
 KM Biomineralization; Hydrolase; Metalloprotease; Zinc; Signal-anchor;  
 KW Transmembrane; Glycoprotein.  
 FT DOMAIN 1 20  
 FT TRANSMEM 21 37  
 FT DOMAIN 1 37  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 580 581  
 FT METAL 584 584  
 FT METAL 642 642  
 FT ACT SITE 646 646  
 FT CARBOHYD 71 71  
 FT CARBOHYD 238 238  
 FT CARBOHYD 263 263  
 FT CARBOHYD 290 290  
 FT CARBOHYD 301 301  
 FT CARBOHYD 377 377  
 FT CARBOHYD 484 484  
 FT CARBOHYD 736 736  
 FT CONFLICT 430 430  
 SQ SEQUENCE 749 AA; 86418 MW; A88FA481C376C18A CRC64;  
 D -> V (IN REF. 3).

Query Match 28.2%; Score 1207; DB 1; Length 749;  
 Best Local Similarity 35.3%; Pred. No. 3.6e-73;  
 Matches 264; Conservative 145; Mismatches 299; Indels 40; Gaps 19;

Qy 93 KGRQLLSRFTOLEVLVAGSLLAALLGCVAVGVYHRDPSSHSTCLTEACIRVAGKI 152  
 Db 13 KGRNR-GIRALMLFI-GTLVIGTLIF-LVSGGLSPQ-ANGCYLCKRECEIAAAAI 66  
 Qy 153 LESLDGVSPCEDPYQSCGGMIRNPLPDGRSRNNTNSIMDNOAILKHLN-NTTFN 211  
 Db 67 MSKVMLSVDPENEFRAFCDGMSINNPIDEMPSGVGVPMIRHNVLDLKALLESVSR 126  
 Qy 212 SSSSEACKTORFYVSCLOVERIEELGQPLRLDLKIK-GNNI-----GPMDDNF- 262  
 Db 127 RDTENVQAKILYSSCMKEKALEKADAPLHLHSHFRPVLEANGPQVMSERKFS 186  
 Qy 263 -MEVLKAVAGTYRATPEFTVYISADSKSSNSVIOVDSGLFLPSRDYANIRANEXVLT 321  
 Db 187 LLQTLATRGQVNSVFIKLVVSPDDKASNHILKLDQATLSLAVREDPLDNTTEAK--- 243  
 Qy 322 AYLD---YMEELGMLGGRPTSTREOMQVLELEIQLANITTVQDQDRDEKIYHKSI 377  
 Db 244 SYRDLVYFMDVTVLGLANSRSRAEHDKSVLRLEIKLAELMTPH-ENKRTSEAMVXNI 302  
 Qy 378 SELQALPSMMLLEFLSLSP-----LELSDSPVVVGVMDVLOVSELIINRTPSIL 431  
 Db 303 SELSAMIDQFPLGLYIKKIVITRLYPHLKDIGPSBNVAVRQYFKULFRILGARKKTI 362  
 Qy 432 NNYLIMLVQKTTSLDRPESAOEKLLETIVYTKKSCVPRMOTCISNTDAGPALGSL 491  
 Db 363 ANYLVMRVYSRIPRLSRFYRMLEFERYVIGT-TLLPQMDKCVNRTESALPVVQKM 421  
 Qy 492 FVKATFDROSKELAGMISEIRTAPEEL-QGLVYMDKTRQAAKERADAYIMIGPDP 550  
 Db 422 FVNHFQDCKEMEBELLEGVWAFIDMLEKENMMDAGTRKQAEKRAVALAVGYEF 481  
 Qy 551 ILPEKLEDVYDGYEISEDSFQOMNLNYSKAVMDQLRKPSRDQMSVTPOTVNAVY 610  
 Db 482 IINDTYVEDLKAIFSSDYFGAVLQTRKLAQSDFFMLKAVPKTEWFTNPTTVNAVY 541  
 Qy 611 LPTKNEIVPAGIILQAPY-ARNHPKALNFGAIGVVMGHELTTHAFDDQGREYDKGNLRP 669  
 Db 542 SASVQGIFFPAGELQKPFVWGTEYPRSLSTGALIGVIGHEFTHGDDNNGRKDKGNLDP 601



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 16:38:11 ; Search time 70 Seconds

(without alignments)  
3655.504 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALQELGAGSNMVEYKRA.....RHFGCPVGSFNNPQLCEVW 811

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_ricket:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4281	100.0	811	4 Q8NFD7	Q8NFD7 homo sapien
2	3820	89.2	765	6 Q865C2	Q865C2 bos taurus
3	3772	88.1	816	6 Q865C4	Q865C4 bos taurus
4	3695	86.3	763	11 Q923T6	Q923T6 mus musculus
5	3665	85.6	763	11 Q80257	Q80257 mus musculus
6	3659.5	85.5	736	6 Q865C3	Q865C3 bos taurus
7	3624	84.7	814	11 Q80259	Q80259 mus musculus
8	3572.5	83.5	785	11 Q80260	Q80260 mus musculus
9	3556	83.1	734	11 Q80258	Q80258 mus musculus
10	3371	78.7	709	11 Q8C099	Q8C099 mus musculus
11	2653	62.0	752	13 Q9DGM6	Q9DGM6 gallus galli
12	2574	60.1	752	13 Q7ZTK3	Q7ZTK3 xenopus lae
13	2554	59.7	758	6 Q28868	Q28868 bos taurus
14	2546	59.5	758	6 Q28010	Q28010 bos taurus
15	2352.5	55.0	526	11 Q8K0P0	Q8K0P0 mus musculus
16	1810	42.3	727	5 Q81S64	Q81S64 locusta mlg

17	1647	38.5	786	5 Q9W5Y0	Q9W5Y0 drosophila
18	1647	38.5	786	5 Q8W5S1	Q8W5S1 drosophila
19	1521	35.5	849	5 Q9W436	Q9W436 drosophila
20	1452	33.9	770	4 Q96PH9	Q96PH9 homo sapien
21	1442.5	33.7	742	11 Q9ERK3	Q9ERK3 mus musculus
22	1431	33.4	765	11 Q9JL13	Q9JL13 mus musculus
23	1430.5	33.4	742	11 Q9QZV6	Q9QZV6 mus musculus
24	1427	33.3	779	11 Q9ERK2	Q9ERK2 mus musculus
25	1419	33.1	765	11 Q9QZV7	Q9QZV7 mus musculus
26	1398.5	32.7	845	4 Q86TH4	Q86TH4 homo sapien
27	1373.5	32.1	976	5 Q91714	Q91714 drosophila
28	1373.5	32.1	1040	5 Q8T062	Q8T062 drosophila
29	1321	30.9	770	5 Q9U9P2	Q9U9P2 hydra attenu
30	1290.5	30.1	750	11 Q8K251	Q8K251 mus musculus
31	1290	30.1	848	5 Q16796	Q16796 caenorhabdi
32	1287.5	30.1	772	5 Q86RS4	Q86RS4 manduca sex
33	1277.5	29.8	772	5 Q9BLH1	Q9BLH1 bombyx mori
34	1264	29.5	770	13 Q93394	Q93394 perca flav
35	1208.5	28.2	736	5 Q44857	Q44857 caenorhabdi
36	1204	28.1	749	11 Q35812	Q35812 rattus norv
37	1199.5	28.0	766	5 Q18673	Q18673 caenorhabdi
38	1197	28.0	763	5 Q9X201	Q9X201 drosophila
39	1168	27.3	816	5 Q81T23	Q81T23 caenorhabdi
40	1137.5	26.6	739	5 Q8T660	Q8T660 venturia ca
41	1096	25.6	787	5 Q9UA44	Q9UA44 aplysia cal
42	972.5	22.7	713	11 Q9E0R2	Q9E0R2 mus musculus
43	945.5	22.1	665	17 Q8T9B2	Q8T9B2 methanocarc
44	937	21.9	754	5 Q19831	Q19831 caenorhabdi
45	934	21.8	694	16 Q8EAQ3	Q8EAQ3 shewanella

## ALIGNMENTS

RESULT 1

Q8NFD7 PRELIMINARY, PRT, 811 AA.

Q8NFD7

01-OCT-2002 (TRENBLREL. 22, Created)

01-OCT-2002 (TRENBLREL. 22, Last sequence update)

01-OCT-2003 (TRENBLREL. 25, Last annotation update)

Endothelin-converting enzyme-2C.

GN ECE2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE:Thalamus; Scheuch K., Behrouzi T., Synowitz M., Draheim N.,

RA Funke-Kaiser B., Thomas A., Zollmann F.S., Paul M., Orzechowski H.D.;

RA Schwaneberg B., "Human endothelin-converting enzyme-2C (ECE-2C): a new ECE-2

RT variant.";

RT Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.

RI EMBL, AF521189; AAM77664.1; .

DR GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.

DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.

DR GO; GO:0008270; F:zinc ion binding; ISS.

DR GO; GO:0007420; P:brain development; ISS.

DR GO; GO:0010002; P:cardioblast differentiation; ISS.

DR GO; GO:0007267; P:cell-cell signaling; ISS.

DR GO; GO:0009790; P:embryonic development; ISS.

DR GO; GO:0007507; P:heart development; ISS.

DR GO; GO:0016486; P:peptide hormone processing; ISS.

DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.

DR GO; GO:0042310; P:vasoconstriction; ISS.

DR InterPro; IPR000718; Peptidase\_M13.

DR InterPro; IPR008753; Peptidase\_M13\_N.

DR InterPro; IPR006025; Pept\_M2n\_BS.

DR InterPro; IPR000221; Protamine\_P1.

DR Pfam; PF01431; Peptidase\_M13; 1.

DR Pfam; PF05649; Peptidase\_M13\_N; 1.

DR PRINTS; PRO0786; NEPRILYSIN.  
 DR PROSITE; PS00048; PROTAINE PL; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 SO SEQUENCE 811 AA; 91211 MW; 73797FAEA937FCE CRC64;

Query Match 100.0%; Score 4281; DB 4; Length 811;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-301;  
 Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNVALQELGAGSNMVEYKATLRDADAPETVEGASPDANVEKGASPFSPGSPGNT 60
DB 1 MNVALQELGAGSNMVEYKATLRDADAPETVEGASPDANVEKGASPFSPGSPGNT 60
QY 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
DB 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
QY 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
DB 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
QY 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 180
DB 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 180
QY 181 PDGRSRMNTFNSLMDQNALIKHLLENTTFFNSSSEAEOKTQRFYLSCLQVERIEELGAP 240
DB 181 PDGRSRMNTFNSLMDQNALIKHLLENTTFFNSSSEAEOKTQRFYLSCLQVERIEELGAP 240
QY 241 LRDLIEKIGMNIITGPMQDNFMEVLKAVAGTYRATPFTYVISADEKSSNSNVIQVDS 300
DB 241 LRDLIEKIGMNIITGPMQDNFMEVLKAVAGTYRATPFTYVISADEKSSNSNVIQVDS 300
QY 301 GLFLPSRDYILNRTANEKVLTAIYLDYMEELGMLGGRPTSTRBQOVLLEIOLANITV 360
DB 301 GLFLPSRDYILNRTANEKVLTAIYLDYMEELGMLGGRPTSTRBQOVLLEIOLANITV 360
QY 361 PODQRDEBKLYHKMSISELOALAPSDMLEFSLSPLELSDSEPPVYVGMQYLQVDS 420
DB 361 PODQRDEBKLYHKMSISELOALAPSDMLEFSLSPLELSDSEPPVYVGMQYLQVDS 420
QY 421 ELINRTESILNNYILNMLVOKTSSLDRRFESAQEKLETLVGTKKSCVPRMOTCISNT 480
DB 421 ELINRTESILNNYILNMLVOKTSSLDRRFESAQEKLETLVGTKKSCVPRMOTCISNT 480
QY 481 DDALGFALGSLFVKATPDROSKELAEGMISEIRTAPEEALGOLVWMDKTRQAAEKADA 540
DB 481 DDALGFALGSLFVKATPDROSKELAEGMISEIRTAPEEALGOLVWMDKTRQAAEKADA 540
QY 541 IYDMIGFDFILPEKELDDVDYGEISBDSFFQNNMLYNFSAKYMADQLAKPSPRDQMS 600
DB 541 IYDMIGFDFILPEKELDDVDYGEISBDSFFQNNMLYNFSAKYMADQLAKPSPRDQMS 600
QY 601 MTPQTVNAVYLLPTKNEIYFPAIGIOLAPYARNHPALNFGIGVVMGHELTHTAFDQRE 660
DB 601 MTPQTVNAVYLLPTKNEIYFPAIGIOLAPYARNHPALNFGIGVVMGHELTHTAFDQRE 660
QY 661 YDKENINLAPWQNEISLAPRNHTACMEQYNOYOUNGRILNORQLGNIAIDNGELKAY 720
DB 661 YDKENINLAPWQNEISLAPRNHTACMEQYNOYOUNGRILNORQLGNIAIDNGELKAY 720
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVGFAGQWCVSTPSSHEGLVTDPHSAPRRV 780
DB 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVGFAGQWCVSTPSSHEGLVTDPHSAPRRV 780
QY 781 LGTLSNSRDFLHFGCPVGSPPMNPQOLCEW 811
DB 781 LGTLSNSRDFLHFGCPVGSPPMNPQOLCEW 811

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## RESULT 2

Q865C2 PRELIMINARY; PRT; 765 AA.  
 AC Q865C2;  
 DT 01-JUN-2003 (Tremblrel. 24, Created)  
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Endothelin-converting enzyme 2b-2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ikeda S., Emoto N., Aikawa J., Yokoyama M., Matsuo M.,  
 RT "Bovine ECE-2b-2";  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF49576; A072363.1; -  
 DR GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.  
 DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.  
 DR GO; GO:0008270; F:zinc ion binding; ISS.  
 DR GO; GO:0007420; P:brain development; ISS.  
 DR GO; GO:0010002; P:cardioblast differentiation; ISS.  
 DR GO; GO:0007267; P:cell-cell signaling; ISS.  
 DR GO; GO:0009780; P:embryonic development; ISS.  
 DR GO; GO:0007507; P:heart development; ISS.  
 DR GO; GO:0016486; P:peptide hormone processing; ISS.  
 DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.  
 DR GO; GO:0042310; P:vasoconstriction; ISS.  
 DR InterPro; IPR000719; Peptidase M3.  
 DR InterPro; IPR006025; Pept\_M3n\_BS.  
 DR InterPro; IPR000221; Protamine PL.  
 DR Pfam; PF01431; Peptidase M3; 1.  
 DR PRINTS; PRO0786; NEPRILYSIN.  
 DR PROSITE; PS00048; PROTAINE PL; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; 1.  
 SO SEQUENCE 765 AA; 86243 MW; 12C3FE747881E1FP CRC64;

Query Match 89.2%; Score 3820; DB 6; Length 765;  
 Best Local Similarity 89.5%; Pred. No. 7.9e-268;  
 Matches 726; Conservative 17; Mismatches 22; Indels 46; Gaps 1;

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QY 1 MNVALQELGAGSNMVEYKATLRDADAPETVEGASPDANVEKGASPFSPGSPGNT 60
DB 1 MNVALQELGAGSNMVEYKATLRDADAPETVEGASPDANVEKGASPFSPGSPGNT 60
QY 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
DB 61 GTPRSSGLFWRVTCPLHSISGLCSRTWVGFGKGTROLLGSRTOLELVLAGASILLALL 120
QY 43 -----AGRKATSRILGHTLOLELVLAGASILLALL 74
DB 43 -----AGRKATSRILGHTLOLELVLAGASILLALL 74
QY 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 180
DB 121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 180
QY 75 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 134
DB 75 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILBSIDRGVSPCEDPYPGSCGGMIRNPL 134
QY 181 PDGRSRMNTFNSLMDQNALIKHLLENTTFFNSSSEAEOKTQRFYLSCLQVERIEELGAP 240
DB 181 PDGRSRMNTFNSLMDQNALIKHLLENTTFFNSSSEAEOKTQRFYLSCLQVERIEELGAP 240
QY 241 LRDLIEKIGMNIITGPMQDNFMEVLKAVAGTYRATPFTYVISADEKSSNSNVIQVDS 300
DB 241 LRDLIEKIGMNIITGPMQDNFMEVLKAVAGTYRATPFTYVISADEKSSNSNVIQVDS 300
QY 300 IYDMIGFDFILPEKELDDVDYGEISBDSFFQNNMLYNFSAKYMADQLAKPSPRDQMS 600
DB 300 IYDMIGFDFILPEKELDDVDYGEISBDSFFQNNMLYNFSAKYMADQLAKPSPRDQMS 600
QY 601 MTPQTVNAVYLLPTKNEIYFPAIGIOLAPYARNHPALNFGIGVVMGHELTHTAFDQRE 660
DB 601 MTPQTVNAVYLLPTKNEIYFPAIGIOLAPYARNHPALNFGIGVVMGHELTHTAFDQRE 660
QY 661 YDKENINLAPWQNEISLAPRNHTACMEQYNOYOUNGRILNORQLGNIAIDNGELKAY 720
DB 661 YDKENINLAPWQNEISLAPRNHTACMEQYNOYOUNGRILNORQLGNIAIDNGELKAY 720
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVGFAGQWCVSTPSSHEGLVTDPHSAPRRV 780
DB 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVGFAGQWCVSTPSSHEGLVTDPHSAPRRV 780
QY 781 LGTLSNSRDFLHFGCPVGSPPMNPQOLCEW 811
DB 781 LGTLSNSRDFLHFGCPVGSPPMNPQOLCEW 811

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Db 495 IYDMIGFDPFILEPKELIDVYDGYEVSDFQNMNLNLYFSAKWADQARKPSRDQNS 554
QY 601 MRPQTNAYATLPKKEIVPPAGLLOAPFAKRNPKALNFGGIGVWNGHELTHAFDDQGE 660
Db 555 MRPQTNAYATLPKKEIVPPAGLLOAPFYCNHPQALNFGGIGVWNGHELTHAFDDQGE 614
QY 661 YDEKGNLRPMWQNESLAAPFNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAAY 720
Db 615 YDEKGNLRPMWQNESLAAPFNHTACMEBOYSQYQVNGERLNGRQTLGENIADNGGLKAAY 674
QY 721 NAYKAMLRKHGEQOLPAVGLTNHOLFVFGFAQVWCSVTPRESSHGLVTDPHSPARFVY 780
Db 675 NAYKAMLRKHGEQOLPAVGLTNHOLFVFGFAQVWCSVTPRESSHGLVTDPHSPARFVY 734
QY 781 LGTLSNSRDFLRHFGCPVSGPMNPGQLCEVW 811
Db 735 LGTLSNSRDFLRHFGCPVSGPMNPGQLCEVW 765

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## RESULT 3

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O865C4 PRELIMINARY; PRT; 816 AA.
ID Q865C4
AC Q865C4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2a-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]

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SEQUENCE FROM N.A.
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Bovine ECE-2a-2."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF489574; AAO72361.1; -.
DR GO; GO:0030659; Cytoplasmic vesicle membrane; ISS.
DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0007420; P:brain development; ISS.
DR GO; GO:0010002; P:cardioblast differentiation; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0007907; P:embryonic development; ISS.
DR GO; GO:0007507; P:heart development; ISS.
DR GO; GO:0016486; P:peptide hormone processing; ISS.
DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.
DR GO; GO:0042310; P:vasoconstriction; ISS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000221; Proctamine_P1.
DR Pfam; PF01431; Peptidase_M13; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
DR PROSITE; PS00142; ZINC_PROTASEF; 1.
SQ SEQUENCE 816 AA; 92072 MW; BC0DD8FA062672DE CRC64;

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Query Match 88.1%; Score 3772; DB 6; Length 816;
Best Local Similarity 89.5%; Pred. No. 2,7e-264;
Matches 716; Conservative 18; Mismatches 20; Indels 46; Gaps 1;

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QY 12 SNMVEYKATLDEDEAPETPVYVGASPDAMVYKGAAPSPPSPGPMGTGTPRSSGLFWR 71
Db 63 NEMVEYKATLDEDEAPETPVYVGASPDAMVYKGAAPSPPSPGPMGTGTPRSSGLFWR 93
QY 72 VTCPLHRSISGLCSRTMVGOKTRQLGSRQLLEVLGASILLAAALLGCVLALGVQY 131
Db 94 -----AGFRKRTSLLGLHQLLEVLVGLVSLLAALLGLCVLALGVQY 136
QY 132 HDPSSHSTCLTRACIRVACKILLESIDRGVSPCEDFYQSGCGWIRRNPLPDGRSRWNTFN 191

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Db 137 HDPSSHSTCLTRACIRVACKILLESIDRGVSPCEDFYQSGCGWIRRNPLPDGRSRWNTFN 196
QY 192 SIMDNOQALILKILLETNTSSSSSEAEQRTQRYLSTQYERIBELGAQOLRLIETKIGW 251
Db 197 SIMDNOQALILKILLETNTSSSSSEAEKRTQRYLSTQYERIBELGAHRLRLIDIKIGW 256
QY 252 NITGPMDDQNFMEVYKAVGATRPFFTVYISADSKSSNSNVIOVDSGLFAPSADYTL 311
Db 257 NTGPMDDQNFMEVYKAVGATRPFFTVYISADSKSSNSNVIOVDSGLFAPSADYTL 316
QY 312 NRTANEKVLTAALDYMEELGMLLGRPTSTREBQOQVLELEIOLANITVPQDRDEKTI 371
Db 317 NRTANEKVLTAALDYMEELGMLLGGQPTSTREBQOQVLELEIOLANITVPQDRDEKTI 376
QY 372 YHKMSISELQALAPSDMIEFLSPILSPILSDSEPVVYVYVGYNDYIQOVSSELINRTEPSIL 431
Db 377 YHKMSIAELQALAPSDMIEFLSPILSPILSDSEPVVYVYVGYNDYIQOVSSELINRTEPSYL 436
QY 432 NNVLIMNLVQKTTSSIDRRFESAOEKLLETLVGTKSCVPRMOTCISNTDDALGFALGSL 491
Db 437 NNVLIMNLVQKTTSSIDRRFESAOEKLLETLVGTKSCVPRMOTCISNTDDALGFALGSL 496
QY 492 FYKATFDRQSKELIAGMISEIRTAFAEALGQVWMDKTRQAKAKADAIYDMIGPDPRI 551
Db 497 FYKATFDRQSKELIAGMISEIRTAFAEALGHLVWMDKTRQAKAKADAIYDMIGPDPRI 556
QY 552 IEPKELIDVYDGYEVSDFQNMNLNLYFSAKWADQARKPSRDQNSMTQYTNAYTL 611
Db 557 IEPKELIDVYDGYEVSDFQNMNLNLYFSAKWADQARKPSRDQNSMTQYTNAYTL 616
QY 612 PTKNEIVPPAGLLOAPFYABRNPKALNFGGIGVWNGHELTHAFDDQAGREYDEKGNLRPMW 671
Db 617 PTKNEIVPPAGLLOAPFYTCNHPQALNFGGIGVWNGHELTHAFDDQAGREYDEKGNLRPMW 676
QY 672 QNESLAAPFNHTACMEBOYNOYQVNGERLNGRQTLGENIADNGGLKAAYNAYKAMLRKHG 731
Db 677 QNESLAAPFNHTACMEBOYSQYQVNGERLNGRQTLGENIADNGGLKAAYNAYKAMLRKHG 736
QY 732 BEQOLPAVGLTNHOLFVFGFAQVWCSVTPRESSHGLVTDPHSPARFVLTGTLNSRDEL 791
Db 737 BEQOLPAVGLTNHOLFVFGFAQVWCSVTPRESSHGLVTDPHSPARFVLTGTLNSRDEL 796
QY 792 RHRGCPVSGPMNPGQLCEVW 811
Db 797 RHRGCPVSGPMNPGQLCEVW 816

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## RESULT 4

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O923T6 PRELIMINARY; PRT; 763 AA.
ID O923T6
AC O923T6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Endothelin converting enzyme-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

```

```

SEQUENCE FROM N.A.
RA Pan H., Zhanavira N., Devi L.A.;
RT "Mouse Endothelin Converting Enzyme-2 cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF396699; AAK3919.1; -.
DR MEROPS; M13.003; -.
DR MGD; MGI:1101356; Ece2.
DR GO; GO:0030659; Cytoplasmic vesicle membrane; ISS.
DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0007420; P:brain development; IMP.

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DR GO:0010002; P:cardioblast differentiation; IMP.
DR GO:0007267; P:cell-cell signaling; ISS.
DR GO:0009790; P:embryonic development; ISS.
DR GO:0007507; P:heart development; IMP.
DR GO:0016486; P:peptide hormone processing; ISS.
DR GO:0008277; P:regulation of G-protein coupled receptor pr. . .; ISS.
DR GO:0042310; P:vasoconstriction; ISS.
DR InterPro: IPR00718; Peptidase_M13.
DR InterPro: IPR008753; Peptidase_M13_N.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR000221; Procamine_P1.
DR Pfam: PF01431; Peptidase_M13_N.1.
DR Pfam: PF05649; Peptidase_M13_N.1.
DR PRINTS: PRO0786; NEPRILYSIN.
DR PROSITE: PS00048; PROTAMINE_P1.1.
DR PROSITE: PS00142; ZINC_PROTEASE_P1.1.
SQ SEQUENCE 763 AA; 86205 MW; 4B518B0EF9BE549 CRC64;

Query Match      86.3%; Score 3695; DB 11; Length 763;
Best Local Similarity 86.6%; Pred. No. 9e-259;
Matches 702; Conservative 34; Mismatches 27; Indels 48; Gaps 2;

1 MNVALQELGAGSNMVEYKRAITLREDAPETVEGASPDAMEVGKASPFSPGSPGMP 60
1 MNVALHELGGSNMVEYKRAKLRDESPETVEGATRSLE----- 42
61 GTPRSSGLFWRYTCPHLRISISGLCSRTWGFQKGTROLLGASTOLELVLAGSLIAALL 120
43 -----VFQKRTROLFGSHITQLBELVLAGLIVLAALL 74
121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILLESIDRGVSPEDRYOPSCGGMIRNPL 180
75 LGCLVALMW--HRDPAHSTCVTEACIRVAKILLESIDRGVSPQDYPFQSCGGMIRNPL 132
181 PGRSRMTFNSLMDONQAILKHLLENTFNSSSAEOKTORFYLSCLQVERIEELGAOP 240
133 PGRSRMTFNSLMDONQAILKHLLENTFNSSSAEOKTRSYLSCLQSERIEKGAOP 192
241 LRDLIEKIGGWNITGPMODNFMELKAVAGTYRATPFTTYVISADSKSNSNVIGVDS 300
193 LRDLIKIGGWNITGPMDEDSFMDVYKAVAGTYRATPFTTYVVSADSKSNSNIQVDS 252
301 GLFLPSRDYILNRTANEKYLTAIYDMEELGMLGGRPTSTROMQVLELEIOLANTIV 360
253 GLFLPSRDYILNRTANEKYLTAIYDMEELGVLGGQPTSTROMQVLELEIOLANTIV 312
361 POPORDEEKIYHKSISELQALAPAMDLFLSPLELSDSEPPVYVYGMVLYQVDS 420
313 POPORDEEKIYHKSISELQALAPAVDMLEFLSLPLELSDSEPPVYVYGMVLYQVDS 372
421 ELINRTEPSILNNYLIWNLVQKTTSLDRFESAEKLETLTYGYKSCVPMQTCISNT 480
373 ELINRTEPSILNNYLIWNLVQKTTSLDRFETAEKLETLTYGYKSCVPMQTCISNT 432
481 DDALGALGSLFVKATFEDSKSEIAEGMTSEIRTAEPBALGOLVWMDKETROAKKAKA 540
433 DDALGALGSLFVKATFEDSKSEIAEGMTSEIRTAEPBALGOLVWMDKETROAKKAKA 492
541 IYDMIGFPDFILEPKELDDVYDEYEISEDSFFQNMNLINYNFSAKVADOLRKPSPHDS 600
493 IYDMIGFPDFILEPKELDDVYDEYEISEDSFFQNMNLINYNFSAKVADOLRKPSPHDS 552
601 MTPQYNNAYLLPTKNEIVFPAGILOAPFYARNHPKALNFGIGVNGHELTAAFDQGRE 660
553 MTPQYNNAYLLPTKNEIVFPAGILOAPFYARNHPKALNFGIGVNGHELTAAFDQGRE 612
661 YKREGSLRPMWKNESLAPRNHTACMEBOYNOYUNGERLNGRQTLGENIADNGGLKAY 720
613 YDESGSLRPMWKNESLAPRNHTACMEBOYNOYUNGERLNGRQTLGENIADNGGLKAY 672
721 NAYKATLRKHGEQQLPAVGLTNHQLFVYGAQVMCSVTPRESSHGLVTDPHSPARFV 780
673 NAYKATLRKHGEQQLPAVGLTNHQLFVYGAQVMCSVTPRESSHGLVTDPHSPARFV 732

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QY 781 LGTLSNSRDLFLHFGCGVSSPMNPGOLCEW 811
DB 733 LGTLSNSRDLFLHFGCGVSSPMNPGOLCEW 763

RESULT 5
ID Q80257 PRELIMINARY; PRT; 763 AA.
AC Q80257;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2b-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Mouse ECE-2b-2."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF489572; MA072359.1.
DR GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO:0008270; F:zinc ion binding; ISS.
DR GO:0007420; P:brain development; ISS.
DR GO:0010002; P:cardioblast differentiation; ISS.
DR GO:0007267; P:cell-cell signaling; ISS.
DR GO:0009790; P:embryonic development; ISS.
DR GO:0007507; P:heart development; ISS.
DR GO:0016486; P:peptide hormone processing; ISS.
DR GO:0008277; P:regulation of G-protein coupled receptor pr. . .; ISS.
DR GO:0042310; P:vasoconstriction; ISS.
DR InterPro: IPR00718; Peptidase_M13.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR000221; Procamine_P1.
DR Pfam: PF01431; Peptidase_M13_N.1.
DR PRINTS: PRO0786; NEPRILYSIN.
DR PROSITE: PS00048; PROTAMINE_P1.1.
DR PROSITE: PS00142; ZINC_PROTEASE_P1.1.
SQ SEQUENCE 763 AA; 86457 MW; 2AAND531B32CFC1 CRC64;

Query Match      85.6%; Score 3665; DB 11; Length 763;
Best Local Similarity 86.1%; Pred. No. 1.3e-256;
Matches 698; Conservative 32; Mismatches 33; Indels 48; Gaps 2;

1 MNVALQELGAGSNMVEYKRAITLREDAPETVEGASPDAMEVGKASPFSPGSPGMP 60
1 MNVALHELGGSNMVEYKRAKLRDESPETVEGATRSLE----- 42
61 GTPRSSGLFWRYTCPHLRISISGLCSRTWGFQKGTROLLGASTOLELVLAGSLIAALL 120
43 -----VFQKRTROLFGSHITQLBELVLAGLIVLAALL 74
121 LGCLVALGVQYHRDPSHSTCLTEACIRVAGKILLESIDRGVSPEDRYOPSCGGMIRNPL 180
75 LGCLVALMW--HRDPAHSTCVTEACIRVAKILLESIDRGVSPQDYPFQSCGGMIRNPL 132
181 PGRSRMTFNSLMDONQAILKHLLENTFNSSSAEOKTORFYLSCLQVERIEELGAOP 240
133 PGRSRMTFNSLMDONQAILKHLLENTFNSSSAEOKTRSYLSCLQSERIEKGAOP 192
241 LRDLIEKIGGWNITGPMODNFMELKAVAGTYRATPFTTYVISADSKSNSNVIGVDS 300
193 LRDLIKIGGWNITGPMDEDSFMDVYKAVAGTYRATPFTTYVVSADSKSNSNIQVDS 252
301 GLFLPSRDYILNRTANEKYLTAIYDMEELGMLGGRPTSTROMQVLELEIOLANTIV 360
253 GLFLPSRDYILNRTANEKYLTAIYDMEELGVLGGQPTSTROMQVLELEIOLANTIV 312

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QY 361 PODORDEEKIYHKMSISELQALAPSMWLEFLSLSELESDSEPVVYGVMDYLOQVS 420  
DB 313 PODORDEEKIYHKMSISELQALAPSMWLEFLSLSELESDSEPVVYGVMDYLOQVS 372  
QY 421 ELINTEPSILNNYILWNLVQKTTSSLDPRFSAQKLETLVGTCKSCVPRMOTCISNT 480  
DB 373 ELINTEPSILNNYILWNLVQKTTSSLDPRFSAQKLETLVGTCKSCVPRMOTCISNT 432  
QY 481 DDALCPALGSLFVKATPFDRQSKIEAGMISELRTAFEEALGOLVWMDKTRQAAEKKA 540  
DB 433 DDALCPALGSLFVKATPFDRQSKIEAGMISELRTAFEEALGOLVWMDKTRQAAEKKA 492  
QY 541 IYDMIGFDPFLEPKELDDVYGYEISEDSFQNMNLNFSKAKWADQRRKPSRQDS 600  
DB 493 IYDMIGFDPFLEPKELDDVYGYEISEDSFQNMNLNFSKAKWADQRRKPSRQDS 552  
QY 601 MTPQVNAVYLLPTKNEIVFPAGILQAPYARNHPKALNFGIGVWGHETLAFDDQGE 660  
DB 553 MTPQVNAVYLLPTKNEIVFPAGILQAPYARNHPKALNFGIGVWGHETLAFDDQGE 612  
QY 661 YKKEGNTLRPMWQNESLAFRNTTACMEBOYNOYVNGERLNGRQTLGENTLADNGIKAY 720  
DB 613 YKKEGNTLRPMWQNESLAFRNTTACMEBOYNOYVNGERLNGRQTLGENTLADNGIKAY 672  
QY 721 NAYKAMLRKGGEEQOLPAVGLTNHOLFVGFPAQWCVRTPESSHEGLVTDPHSPARFV 780  
DB 673 NAYKAMLRKGGEEQOLPAVGLTNHOLFVGFPAQWCVRTPESSHEGLVTDPHSPARFV 732  
QY 781 LGTLSNSRDLFNRHFGCPVGSPPMNPQGLCEW 811  
DB 733 LGTLSNSRDLFNRHFGCPVGSPPMNPQGLCEW 763

## RESULT 6

Q865C3 PRELIMINARY; PRT; 736 AA.  
AC Q865C3;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DE Endothelin-converting enzyme 2b-1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
NCBI\_Taxid=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;  
RT "Bovine ECE-2b-1";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AF489575; AA072362.1; -.  
DR GO:GO:0030659; Cytoplasmic vesicle membrane; ISS.  
DR GO:GO:0016511; Endothelin-converting enzyme activity; ISS.  
DR GO:GO:0008270; Zinc ion binding; ISS.  
DR GO:GO:0007420; P:brain development; ISS.  
DR GO:GO:0010002; P:cardioblast differentiation; ISS.  
DR GO:GO:0007267; P:cell-cell signaling; ISS.  
DR GO:GO:0009790; P:embryonic development; ISS.  
DR GO:GO:0016486; P:peptide hormone processing; ISS.  
DR GO:GO:0008277; P:regulation of G-protein coupled receptor pr. .; ISS.  
DR GO:GO:0043310; P:vasoconstriction; ISS.  
DR InterPro: IPR000718; Peptidase\_M13.  
DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro: IPR000221; Proctamine\_P1.  
DR Pfam: PF01431; Peptidase\_M13; 1.  
DR PRINTS: PR00786; NEPRILYSIN.  
DR PROSITE: PS00048; PROCTAMINE\_P1; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
SQ SEQUENCE 736 AA; 83128 NM; 7ECD124469751D91 CRC64;

Query Match

85.5%; Score 3659.5; DB 6; Length 736;

Best Local Similarity 95.3%; Pred. No. 3.2e-256;  
Matches 688; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 90 GFQKTRQLSGSRTOLELVLAGASLLLAALLGCVAGVQYHRPSSHCTCEACIRVA 149  
DB 15 GFRKTRSLGHTLDELVLAVGSLLLAALLGCVAGVQYHRPSSHCTCEACIRVA 74  
QY 150 GKLISLRGVSPCEDPFOGCGMIRRNPLPDGRSMWTFSLMDONAILKHLENT 209  
DB 75 GKLISLRGVSPCEDPFOGCGMIRRNPLPDGRSMWTFSLMDONAILKHLENT 134  
QY 210 FNSSEAEQKTRFYLSCLQVERIEELGAQPLRLDIEKIGNITGPMQDNFMEVLKAV 269  
DB 135 FNSSEAEKTRKTRFYLSCLQVERIEELGHALRDLIDKIGNNVYGPMDQDFMEVLKAV 194  
QY 270 ACTYRATPEFTYVYISADSKSSNSNYIYVDQSLFLPSRDYILNRANERYLTAIYDMEB 329  
DB 195 ACTYRATPEFTYVYISADSKSSNSNYIYVDQSLFLPSRDYILNRANERYLTAIYDMEB 254  
QY 330 LGMILGSRPTSRBOOVLELEIOLANTVPODORDEEKIYHKMSISELQALAPSMW 389  
DB 255 LGMILGSGPTSTRBOOVLELEIOLANTVPODORDEEKIYHKMSIABLQALAPSMW 314  
QY 390 LEFLSLSPLELSDSEPVVYGVMDYLOVSELNRTESILNNYILWNLVQKTTSSLD 449  
DB 315 LEFLSLSPLELSDSEPVVYGVMDYLOVSELNRTESVANNYILWNLVQKTTSSLDH 374  
QY 450 RFESAQKLETLVGTCKSCVPRMOTCISNTDLAGFALGSLFVATFDRQSKIEAGMI 509  
DB 375 RFESAQKLETLVGTCKSCVPRMOTCISNTDLAGFALGSLFVATFDRQSKIEAGMI 434  
QY 510 SEIRTAPEALGOLVWMDKTRQAAEKADALYDMIGPDLFLEPKELDDVYGYEISD 569  
DB 435 SEIRTAPEALGOLVWMDKTRQAAEKADALYDMIGPDLFLEPKELDDVYGYEISD 494  
QY 570 SFQNMNLNFSKAKWADQRRKPSRQDSMTPQVNAVYLLPTKNEIVFPAGILQAPRY 629  
DB 495 SFQNMNLNFSKAKWADQRRKPSRQDSMTPQVNAVYLLPTKNEIVFPAGILQAPRY 554  
QY 630 ANRHPKALNFGIGVWGHETLAFDDQREYDEKGNLRPMWQNTSLAFRNHTACMEQ 689  
DB 555 TCNHPQALNFGIGVWGHETLAFDDQREYDEKGNLRPMWQNTSLAFRNHTACMEQ 614  
QY 690 YNOYVNGERLNGRQTLGENTLADNGIKAAVNAVYAMLRKGGEEQOLPAVGLTNHOLFV 749  
DB 615 YNOYVNGERLNGRQTLGENTLADNGIKAAVNAVYAMLRKGGEEQOLPAVGLTNHOLFV 674  
QY 750 GFAQWCVRTPESSHEGLVTDPHSPARFVYLGTLNSRDLFNRHFGCPVGSPPMNPQGLCE 809  
DB 675 GFAQWCVRTPESSHEGLVTDPHSPARFVYLGTLNSRDLFNRHFGCPVGSPPMNPQGLCE 734

## RESULT 7

Q80259 PRELIMINARY; PRT; 814 AA.  
AC Q80259;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DE Endothelin-converting enzyme 2a-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;  
RT "Mouse ECE-2a-2";



```

QY 301 GFLPSRDYLRNRTANEKVLTAVIDMEELGMLGRPTSTREOMQOVLLEIQLANITY 360
DB 275 GFLPSRDYLRNRTANEKVLTAVIDMEELGMLGRPTSTREOMQOVLLEIQLANITY 334
QY 361 PODQDRDEEKIYHKMSISELQALAPSMWLSEFLSPLEISDSSEPVVYVGMVLYQVVS 420
DB 335 PODQDRDEEKIYHKMSISELQALAPSMWLSEFLSPLEISDSSEPVVYVGMVLYQVVS 394
QY 421 ELINTEPSILNNYILWNIVOKTSSLDLRFESAOKLETLTYGTCKSCVPRMOTCISMT 480
DB 395 ELINTEPSILNNYILWNIVOKTSSLDLRFESAOKLETLTYGTCKSCVPRMOTCISMT 454
QY 481 DDALGALGSLFVKAFTPDQSKIEAEGMISEIRTAEEALGOLVWMDKTRQAKKAXA 540
DB 455 DDALGALGSLFVKAFTPDQSKIEAEGMISEIRTAEEALGOLVWMDKTRQAKKAXA 514
QY 541 IYDMIGFPDILPEKELDDVDYGYEISEDSFQNMMLNLYNFSKAVADQLRKPSRDQVS 600
DB 515 IYDMIGFPDILPEKELDDVDYGYEISEDSFQNMMLNLYNFSKAVADQLRKPSRDQVS 574
QY 601 MTPQYVNAAYLPTKNEIVPAGILQAPFPAKRNPKALNFGGIGVWGHGELTHAFDQGR 660
DB 575 MTPQYVNAAYLPTKNEIVPAGILQAPFPAKRNPKALNFGGIGVWGHGELTHAFDQGR 634
QY 661 YKEGNLRPMWONESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGLKAAY 720
DB 635 YKEGNLRPMWONESLAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGLKAAY 694
QY 721 NAYKAMLRKGEQOLPAVGLTNHQLFVYGAQVWCVRTPESHEGLVTDPHSPARFV 780
DB 695 NAYKAMLRKGEQOLPAVGLTNHQLFVYGAQVWCVRTPESHEGLVTDPHSPARFV 754
QY 781 LGTILNSRDLRHFPGCVGSPMNPGLCEW 811
DB 755 LGTILNSRDLRHFPGCVGSPMNPGLCEW 785

RESULT 9
ID Q80258 PRELIMINARY; PRT; 734 AA.
AC Q80258;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin-converting enzyme 2b-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Ikeda S., Emoto N., Ikeda K., Yokoyama M., Matsuo M.;
RT "Mouse ECE-2b-1."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF489571; AAC02358.1; -
DR GO; GO:0030659; C:cytoplasmic vesicle membrane; ISS.
DR GO; GO:0016511; F:endothelin-converting enzyme activity; ISS.
DR GO; GO:0008270; F:zinc ion binding; ISS.
DR GO; GO:0007420; P:brain development; ISS.
DR GO; GO:0010002; P:cardioblast differentiation; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0007907; P:myogenic development; ISS.
DR GO; GO:0007507; P:heart development; ISS.
DR GO; GO:0016486; P:regulation of G-protein coupled receptor pr. .; ISS.
DR GO; GO:0042310; P:vasoconstriction; ISS.
DR InterPro; IPR000718; Peptidase_M13.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF01431; Peptidase_M1; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00048; PROTAMINE_P1; 1.

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DR PROSITE; PS00142; ZINC PROTEASE; 1.
SQ SEQUENCE 734 AA; 83066 MW; 00DA7AD1F72D5D8 CRC64;
Query Match 83.1%; Score 3556; DB 11; Length 734;
Best Local Similarity 92.7%; Pred. No. 1e-248;
Matches .670; Conservative 26; Mismatches 25; Indels 2; Gaps 1;
QY 69 VGFQKTRQLGSRQLBELVLAGASLLAALLGLCLVAGVQYHRDPHSSTCLTEACTIV 148
DB 14 VGFQKTRQLGSRQLBELVLAGLILVLAALLGLCLVLAIV--HNDPASTCVTEACTIV 71
QY 149 AKGILLESIDRGVSPCEDFYQFSCGGMIRRNPLPDGRSRMNTFNLSMDQNALIKHLNLT 208
DB 72 AKGILLESIDRGVSPQDFYQFSCGGMIRRNPLPNGRSRMNTFNLSMDQNALIKHLNLT 131
QY 209 TNNSSSEAEQKTRFYLLSCLQVERIIEBGAQPLRLIEKIGMNITGPMDDNFMELKA 268
DB 132 TNNSSSEAEKTRSFYLLSCLQSERIEKLGAKPLRLIDIKIGMNITGPMDEDSFMDVLKA 191
QY 269 VAGTRATPEFTVYISADSKSNSNVIOVDSGLFLPSRDYLRNRTANEKVLTAVIDYV 328
DB 192 VAGTRATPEFTVYISADSKSKYSNITVDQSGFLPSRDYLRNRTANEKVLTAVIDYV 251
QY 329 ELGMLLGRGPTSTREOMQOVLLEIQLANITYPOQDRDEEKIYHKMSISELQALAPSM 388
DB 252 ELGMLLGRGPTSTREOMQOVLLEIQLANITYPOQDRDEEKIYHKMSISELQALAPSM 311
QY 389 WLEFLSPLEISDSSEPVVYVGMVLYQVSELINTEPSILNNYILWNIVOKTSSLD 448
DB 312 WLEFLSPLEISDSSEPVVYVGMVLYQVSELINTEPSILNNYILWNIVOKTSSLD 371
QY 449 RPESAOKLETLTYGTCKSCVPRMOTCISNTDDALGALGSLFVKAFTPDQSKIEAEGM 508
DB 372 RPESAOKLETLTYGTCKSCVPRMOTCISNTDDALGALGSLFVKAFTPDQSKIEAEGM 431
QY 509 ISEIRTAEEALGOLVWMDKTRQAKKAXAIYDMIGFPDILPEKELDDVDYGYEISE 568
DB 432 ISEIRTAEEALGOLVWMDKTRQAKKAXAIYDMIGFPDILPEKELDDVDYGYEISE 491
QY 569 DSFPQNMMLNLYNFSKAVADQLRKPSRDQVMTQYVNAAYLPTKNEIVPAGILQAPF 628
DB 492 DSFPQNMMLNLYNFSKAVADQLRKPSRDQVMTQYVNAAYLPTKNEIVPAGILQAPF 551
QY 629 YARNRPKALNFGGIGVWGHGELTHAFDQGRYDREGNLRPMWONESLAFRNHTACME 688
DB 552 YARNRPKALNFGGIGVWGHGELTHAFDQGRYDREGNLRPMWONESLAFRNHTACME 611
QY 689 QYNOYVNGERLNGRQTLGENIADNGLKAAYNAKYAMLKRGGEQOLPAVGLTNHQLPF 748
DB 612 QYNOYVNGERLNGRQTLGENIADNGLKAAYNAKYAMLKRGGEQOLPAVGLTNHQLPF 671
QY 749 VGFQVWCVRTPESHEGLVTDPHSPARFVLTGLTILNSRDLRHFPGCVGSPMNPGLQC 808
DB 672 VGFQVWCVRTPESHEGLVTDPHSPARFVLTGLTILNSRDLRHFPGCVGSPMNPGLQC 731
QY 809 EYW 811
DB 732 EYW 734

RESULT 10
ID Q8C099 PRELIMINARY; PRT; 709 AA.
AC Q8C099;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endothelin converting enzyme-2 homolog.
GN ECE2 OR 6330509A19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The PANTOM Consortium,  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team,  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK031951; BAC27618.1; -.  
 DR MGD; MGI:1101356; Ece2.  
 DR GO; GO:0030659; Cytoplasmic vesicle membrane; ISS.  
 DR GO; GO:0016511; F-actin binding; ISS.  
 DR GO; GO:0008270; F-actin ion binding; ISS.  
 DR GO; GO:0007420; P. brain development; ISS.  
 DR GO; GO:0010002; P. cardioblast differentiation; ISS.  
 DR GO; GO:0007267; P. cell-cell signaling; ISS.  
 DR GO; GO:0007507; P. embryonic development; ISS.  
 DR GO; GO:0007507; P. heart development; ISS.  
 DR GO; GO:0016486; P. peptide hormone processing; ISS.  
 DR GO; GO:0008277; P. regulation of G-protein coupled receptor pr. .; ISS.  
 DR GO; GO:0042310; P. vasocostriction; ISS.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF01431; Peptidase\_M13\_1.  
 DR Pfam; PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 709 AA; 80252 MW; 68815C0DA949C8FA CRC64;

Query Match 78.7%; Score 3371; DB 11; Length 709;

Best Local Similarity 85.5%; Pred. No. 2.4e-235;

Matches 645; Conservative 33; Mismatches 28; Indels 48; Gaps 2;

QY 1 MNAVALDELGASNMVEYKATLTDEDAPEYFGGASPDAMEYKASPPSPSPGKMP 60  
 DB 1 MNAVALHELGGGSGMVEYKAKLDESPETIVGRATRSLE----- 42  
 QY 61 GTPRSGLFWRVTCPLHRSISGLCSRTMVGFGKTRQLQSGRTQLEVLVAGSLTALL 120  
 DB 43 -----VGFQRTQLQFESHQLEVLVAGSLTALL 74  
 QY 121 LGLVALGVQYHRDPHSSTCLTEACIRVAKKILESIDRGVSPCEDFYQSGCGMIRNP 180  
 DB 75 LGLVALVMV--HRDPASTCVTEACIRVAKKILESIDRGVSPCEDFYQSGCGMIRNP 132  
 QY 181 PDRSRKMTNFSAMDQNALIKHLNRTTNSSEAPQKQRYISCLQVRIEELGAQ 240  
 DB 133 PNRSRKMTNFSAMDQNALIKHLNRTTNSSEAPKTRSPYLSCLQSERLEKLGAKP 192  
 QY 241 LRDLEIKGWNITGPMDDNFMVYKAVAGYRAFPFTVYISADSKSSNSVIVQDS 300  
 DB 193 LRDLEIKGWNITGPMDDNFMVYKAVAGYRAFPFTVYISADSKSSNSVIVQDS 252  
 QY 301 GLFLPSRDYVLTNRANKEVLTAVLYDMEELGMLGGPSTREMOQVLELITQANITY 360  
 DB 253 GLFLPSRDYVLTNRANKEVLTAVLYDMEELGMLGGPSTREMOQVLELITQANITY 312  
 QY 361 PQQRARDEEKIYKMSISELQALAPSDMEFLSPILSPLESDSEPVVYVGMQDIQVS 420  
 DB 313 PQQRARDEEKIYKMSISELQALAPSDMEFLSPILSPLESDSEPVVYVGMQDIQVS 372  
 QY 421 ELINRTSPILNNYILNVLVQKTTSLDRFESAOEKLLETLTGTKS CVPRQTCISNT 480  
 DB 373 ELINRTSPILNNYILNVLVQKTTSLDRFESAOEKLLETLTGTKS CVPRQTCISNT 432  
 QY 481 DDALGPAAGSLFYKATPDRQSKIEAGMISEIRTAFEALGOLVMDDEKTRQAKKAKA 540  
 DB 433 DDALGPAAGSLFYKATPDRQSKIEAGMISEIRTAFEALGOLVMDDEKTRQAKKAKA 492  
 QY 541 IYMGIPPDITLPEKELDYYDGYEISEDFPQMLNLNFSKAVMADQKRPSPDQMS 600

DB 493 IYDMIGPFDILPEPELDVYDGYEISEDFPQMLNLNFSKAKMADQKRPSPDQMS 552  
 QY 601 MTPQTVNAYVYLPKNEIVPAGIILQAPFYARNHPKALNFGSIGVMGHELTAAFDQGRE 660  
 DB 553 MTPQTVNAYVYLPKNEIVPAGIILQAPFYARNHPKALNFGSIGVMGHELTAAFDQGRE 612  
 QY 661 YDKENLRPMQWONSLAFRNHTACMEQYQYQVNGERLNGRQTLGENTADNGLKAY 720  
 DB 613 YDKENLRPMQWONSLAFRNHTACMEQYQYQVNGERLNGRQTLGENTADNGLKAY 672  
 QY 721 NAYKAMLRKGEEOQLPAVGLTNHQLPFVGFPAQV 754  
 DB 673 NAYKAMLRKGEEOQLPAVGLTNHQLPFVGFPAQV 706

## RESULT 11

ID Q9DGN6 PRELIMINARY; PRT: 752 AA.  
 AC Q9DGN6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Endothelin converting enzyme-1.  
 GN ECE-1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 ON NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2036360; PubMed=10903177;  
 RA Takebayashi-Suzuki K., Yanagisawa M., Gourdie R.G., Kanawa N.,  
 RA Mikawa T.;  
 RT "In vivo induction of cardiac Purkinje fiber differentiation by  
 RT coexpression of preproendothelin-1 and endothelin converting enzyme-  
 RT 1.";  
 RL Development 127:3523-3532 (2000).  
 DR EMBL; AF230274; AAF98287.1; -.  
 DR HSSP; P08473; 1DMT.  
 DR MEROPS; M13.002; -.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0008237; P-metallopeptidase activity; IEA.  
 DR GO; GO:004245; P-neprilysin activity; IEA.  
 DR GO; GO:0008270; F-zinc ion binding; IEA.  
 DR GO; GO:0006508; P-proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000718; Peptidase\_M13.  
 DR InterPro; IPR008753; Peptidase\_M13\_N.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF01431; Peptidase\_M13\_1.  
 DR Pfam; PF05649; Peptidase\_M13\_N\_1.  
 DR PRINTS; PR00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 SQ SEQUENCE 752 AA; 84985 MW; 386B3DB7BF900656 CRC64;

Query Match 62.0%; Score 2653; DB 13; Length 752;

Best Local Similarity 61.8%; Pred. No. 2.8e-183;

Matches 494; Conservative 112; Mismatches 145; Indels 48; Gaps 5;

QY 14 MVEYRATLRDADAPETVEGASPDAMEYKASPPSPSPGKMPGTPRSGLFWRV 73  
 DB 1 MVEYRATLRDADAPETVEGASPPSPSPGKMPGTPRSGLFWRV 40  
 QY 74 CPHLSISGLCSRTMVGFGKTRQLQSGRTQLEVLVAGSLTALLLGLVALGVQYHR 133  
 DB 41 -----AQRTRPKQLVANVAVLAVLGLGLVALGVQYHR 74  
 QY 134 DSHSTCLTEACIRVAKKILESIDRGVSPCEDFYQSGCGMIRNPDPGRSRMTNFS 193  
 DB 75 RPP-AVCISEACISVTSSILSDRTVNPCEDFSYACGGMKXANPLPDGHRMGTFFNL 133  
 QY 194 WQONALHGLLENTFNSSSEAEQKQRYISCLQVRIEELGAQPLDLLEIKGWN 253

DB 134 WEHNOQVIMHLENTTANVSSEAEKRAQRYOQACNNESKIEELRAAPLMELIAKLGMMNI 193  
QY 254 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYIYNR 313  
DB 194 TGPWAGDGNATLREVTAAHRISSPFSSVYVYVADSKSSNSNVIQVDSGLFLPSRDYIYNR 253  
QY 314 TANEXVLTAVLDYMEELGMLLGR-PTSTRQEQOVLLELEIOLANTITVPQDQRDEKXI 372  
DB 254 TENEXVLTAVLDYMEELGMLLGR-PTSTRQEQOVLLELEIOLANTITVPQDQRDEKXI 313  
QY 373 HKMSISELOALAPSDMWLEFLSFLSPLSLSDESPVYVYGMVYLOQVSELINTEPSIIN 432  
DB 314 HKMTAGELDLAPAVDMMPFLSTVFYVPELNESEPVVYVYAKEXYLBQVSDLIILATDCKLAN 373  
QY 433 NYLIWNLQKTTSSLDREPSAOKLELTYGTYKSCVPRMOTCISNTDGLPALGSLF 492  
DB 374 NMIWNLVKTSPFLQRFQDAEKKMEVYGTCKCLPRMKCISDTDNNGLFALGAMF 433  
QY 493 VKATPDRQSKELAEGMISIRTAFAEBALGOLVMDKTRQAAKAKADATYDMIGPDPFL 552  
DB 434 VKATPDRQSKELAEGMISIRTAFAEBALGOLVMDKTRQAAKAKADATYDMIGPDPFL 493  
QY 553 EKPELDVYDGYEISDSFQNNMLNLYNSAKYMAQDLKRPSPRQMSMTPTVNAYYLP 612  
DB 494 DSEKELDKVENDYDAVSDLYFENVMQFYNSARVTLADQLKRPVRDQMSMTPTVNAYYSP 553  
QY 613 TNEKIVFPAGIIQAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREVDKGNLAPMW 672  
DB 554 TNEKIVFPAGIIQAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREVDKGNLAPMW 613  
QY 673 NESLAFRNHTACMEBOYNOYQVNGERLNGRQTLGENTADNGLKAAYNAKYLKRGHE 732  
DB 614 NESVEFKROTACMEBOYNOYQVNGERLNGRQTLGENTADNGLKAAYNAKYLKRGHE 673  
QY 733 EQLPAVGLTNNQLFVGFAGQWCSVTRPESHEGLVTPHSPARFVLGTLNSRDLR 792  
DB 674 EQLPAVGLTNNQLFVGFAGQWCSVTRPESHEGLVTPHSPARFVLGTLNSRDLR 733  
QY 793 HFCPPVSPMNPQOLCEW 811  
DB 734 HFCPPVSPMNPQOLCEW 752

RESULT 12

Q72TK3 PRELIMINARY; PRT; 752 AA.

AC Q72TK3; 01-JUN-2003 (TREMblrel. 24, Created)  
DT 01-JUN-2003 (TREMblrel. 24, last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)  
DE Similar to endochelin-converting enzyme 1.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxId=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.,  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC046653; AAH46653.1; -  
DR GO; GO:0016020; Cmembrane; IEA.  
DR GO; GO:0006237; Fimetallopeptidase activity; IEA.  
DR GO; GO:0004245; Fimetallopeptidase activity; IEA.  
DR GO; GO:0008270; Fimetallopeptidase activity; IEA.  
DR GO; GO:0006508; Pimetallopeptidase activity; IEA.  
DR InterPro; IPR000718; Peptidase\_M13.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR Pfam; PF01431; Peptidase\_M13; I.  
DR PRINTS; PR00786; NEPRILYSIN.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
SQ SEQUENCE 752 AA; 85564 MW; 4BA447B8D3C0F674 CRC64;

Query Match 60.1%; Score 2574; DB 13; Length 752;  
Best Local Similarity 58.9%; Pred. No. 1.5e-177;  
Matches 470; Conservative 132; Mismatches 150; Indels 46; Gaps 4;  
QY 14 WEYKATLRDADAEETPEVAGASPDAMEVKGASPFSPSPGMPGTPTPRSSGLFWRYT 73  
DB 1 MSAYKATLRDADAEETPEVAGASPDAMEVKGASPFSPSPGMPGTPTPRSSGLFWRYT 42  
QY 74 CEHLNISGLCSRTWVQKTRQLLGSRTQLELVLAGSLIALLLGLVALVQYHR 133  
DB 43 -----SERTHVEKLLVLLVIMSLGLFMSLLALSQYRN 76  
QY 134 DSHSGLTEACIRVAGKILSLDRGVSPCEPFOFSCGMIRRPDPGRSRMTFNSL 193  
DB 77 --SNRVCSLSCISYSSLSLRLSDSVDCQDFQYSCGMIKGNRPVPGHSGRWGFENL 134  
QY 194 WDQNALIKHLENTTANVSSEAEOKTORFYLSCLQVERIEELGAOPLDLIETIGMMNI 253  
DB 135 WEHNOQVIMHLENTTANVSSEAEOKTORFYLSCLQVERIEELGAOPLDLIETIGMMNI 194  
QY 254 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYIYNR 313  
DB 195 TGPMDQDNMEVYLKAVAGTYRATPEFTYISADSKSSNSNVIQVDSGLFLPSRDYIYNR 254  
QY 314 TANEXVLTAVLDYMEELGMLLGR-PTSTRQEQOVLLELEIOLANTITVPQDQRDEKXI 373  
DB 255 TENEXVLTAVLDYMEELGMLLGR-PTSTRQEQOVLLELEIOLANTITVPQDQRDEKXI 314  
QY 374 KMSISELOALAPSDMWLEFLSFLSPLSLSDESPVYVYGMVYLOQVSELINTEPSIIN 432  
DB 315 KMTAGELDLAPAVDMMPFLSTVFYVPELNESEPVVYVYAKEXYLBQVSDLIILATDCKLAN 374  
QY 434 YLIWNLVQKTTSSLDREPSAOKLELTYGTYKSCVPRMOTCISNTDGLPALGSLFV 493  
DB 375 YLIWNLVQKTTSSLDREPSAOKLELTYGTYKSCVPRMOTCISNTDGLPALGSLFV 434  
QY 494 KATPDRQSKELAEGMISIRTAFAEBALGOLVMDKTRQAAKAKADATYDMIGPDPFL 553  
DB 435 KATPDRQSKELAEGMISIRTAFAEBALGOLVMDKTRQAAKAKADATYDMIGPDPFL 494  
QY 554 EKPELDVYDGYEISDSFQNNMLNLYNSAKYMAQDLKRPSPRQMSMTPTVNAYYLP 612  
DB 495 EKPELDVYDGYEISDSFQNNMLNLYNSAKYMAQDLKRPSPRQMSMTPTVNAYYLP 554  
QY 614 KNEIVFPAGIIQAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREVDKGNLAPMW 672  
DB 555 KNEIVFPAGIIQAPFYARNHPKALNFGGIGVVMGHELTTHAPDQREVDKGNLAPMW 614  
QY 674 EQLPAVGLTNNQLFVGFAGQWCSVTRPESHEGLVTPHSPARFVLGTLNSRDLR 792  
DB 615 ASVEFKROTACMEBOYNOYQVNGERLNGRQTLGENTADNGLKAAYNAKYLKRGHE 733  
QY 794 QOLPAVGLTNNQLFVGFAGQWCSVTRPESHEGLVTPHSPARFVLGTLNSRDLR 793  
DB 675 KLPPLSLGSLNQLFVGFAGQWCSVTRPESHEGLVTPHSPARFVLGTLNSRDLR 734  
QY 794 FQCPVSPMNPQOLCEW 811  
DB 735 FQCPVSPMNPQOLCEW 752

RESULT 13

Q28868 PRELIMINARY; PRT; 758 AA.

AC Q28868; 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)  
DE Endochelin converting enzyme.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;



[illegible]

OY		680	RNHFAACMEEOYNQVANGVERLNGHOTLGENTADNCGLKAAVAAYKAMLRKHGEBOOLPAY	73
DB		627	KQQTACMWEQIGCNTSVANGEPVNGRHTLLSENLADNGLQAARAYQWKKAGAEOTLPYL	686
OY		740	GLTTHOLEFVFPAQWCVCVTRTPESHGELAVTDPHSPAFPRVLGTLSNRDPLRHFGCPVG	799
DB		687	GLTNQLPFLPSFAQWCVGRPPESHEGLITDPHSPFRVIGSI SNSKEFSHFHCPCPG	746
OY		800	SPANPGOLCEYW	811
DB		747	SPANPHHKCEYW	758
 RESULT 14				
ID	Q28010	PRELIMINARY;	PRT;	758 AA.
AC	Q28010;			
DT	01-NOV-1996	(TREMBLrel. 01. Created)		
DT	01-NOV-1996	(TREMBLrel. 01. Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25. Last annotation update)		
DE	Endothelin converting enzyme-1a.			
GN	ECE-1A.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OX	Bovidae; Bovinae; Bos.			
NCBI	_taxid=9913;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=94340737; PubMed=8062389;			
RT	Xu D., Emoto N., Giald A., Slaughter C., Kaw S., dewit D.,			
RT	"ECE-1: a membrane-bound metalloprotease that catalyzes the			
RL	proteolytic activation of big endothelin-1,"			
RN	Cell 78:473-485(1994).			
RP	[2]			
RA	SEQUENCE FROM N.A.			
RL	Yanagisawa M.,			
DR	Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U27342; AAA82928.1; -.			
DR	PIR; A54667; A54667.			
DR	HSSP; P08473; IDMT.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0008237; F:metallopeptidase activity; IEA.			
DR	GO; GO:0004245; F:neprilysin activity; IEA.			
DR	GO; GO:0008270; F:zinc ion binding; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000718; Peptidase_M13_N.			
DR	InterPro; IPR008753; Peptidase_M13_N.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	Pfam; PF01431; Peptidase_M13; 1.			
DR	Pfam; PF05649; Peptidase_M13_N.1.			
DR	PRINTS; PR00786; NEPRILYSIN.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			
SQ	SEQUENCE 758 AA; 85620 MM; 39DCB702099F40A CRC64;			
 Query Match 59.5%; Score 2546; DB 6; length 758; Best Local Similarity 59.8%; Pred. No. 1.6e-175; Matches 474; Conservative 118; Mismatches 160; Indels 40; Gaps 7				
OY		23	RDEDAPERP-VGGASPDAMEVKGKASPSPSPSCMTPTGTPRRSGLFWRVTCPIHLRSIS	81
DB		4	RGODLTRSPPLLGSRAP-----GLTSSPFRLPPSLQVNFRRGNRCRW-----	47
OY		82	GLCSRTWVPQKGTQTLGSRTOLELVLAGASLLAALLLGLVALGVQYH-RDSPSHSTC	140
DB		48	-----AARTPVKRLVTVLALAAALVACLATLVGIQYQRTT--SYC	87
OY		141	LTEACIRVAKILSLDRGVSPCEDFYQSCGWIRRMPLPDGRSRMNTFNSLMDQNAI	200
DB		88	LSSEGISTVSILSMDDPTVDPCCQFFTYAACGWIKANVPDGHSGWGTFSNLMENHOAI	147
OY		201	LKLHLIENTFNSSSAEQTKQRFYVLSCLQVERIEELGAOPLDLLEKIGWNITGWDOD	260



Dh	148	IGHLEENST-ASVSEPERKAQVYYRACMAETRIEELKAKPLMELIEKGGAMNITGGPDKD	206
Qy	261	NEMEVLKAVAGTYRATPFEFTYIISADSKSNSNVIOVDSGLFLPSRDYLYNTANEKYL	320
Dh	207	NFQDTLQVAVTSHYHTSPFESVYVSADSXNSNSNVIOVDSGLFLPSRDYLYNTANEKYL	266
Qy	321	TAIYLYMEELGMLGGRPYST-REMOQVLELEIOLANITVPDQDRDEEKIYHKSISE	379
Dh	267	TGVLNMYVOLGGLLGGGADITRPOQOQILDFETALANITTIPOEKRDEBELIYHKYTAAE	326
Qy	360	LOALPAMDWEFEISLPLSELSDESPVYVGMIDLQOVELINTPEISLNNYLYMNL	439
Dh	327	LOTLPALNMLDFEPLNTIYFVEINSEEPYIYDXEYLSKVSTILNSTDCKLNNYMTMNL	386
Qy	440	VOKTTSILDRRESAOEKLETLTYGSKSCVPRWQTCISNTDAGFALGSLFVKATPDR	499
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Qy	500	QSKETAEKMTSIRTAFEFALGQLYMDEKTRQAEKADAIYDMIGPDPFILEPELDD	559
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Dh	507	VENDTAVPDLTYFENAMRPFNSWRVTAQULRRAPRDMWSMTPPMWNAYSSTKNEIVF	566
Qy	620	PAGIIQAEFYANHPKALNFGGIGVYMGEHETHPFDQGREYDEKGNLSPWONESLAAE	679
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Qy	660	RNHRTACMEQYNOYOVNGERLNGRQTLGENIADNGLKAKAYNAYKAMLRKGEEOQLPAV	739
Dh	627	KQQTCAWGEQYNGYSVNGEPVNGRPHTLGENIADNGLKAKAYRAYQWVVKKNGAEQTLPTL	686
Qy	740	GLTNHQLFPVGAQVWCVVRTPRESSHEGLVTPHPSARPRVGLTNSNRDFLRHFGCPVG	799
Dh	667	GLTNHQLFPFLSGQWCVVRTPRESSHEGLTDPHPSRPRVIGSISNKFESHFHCPCG	746
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DR	GO; GO:0008270; F.zinc ion binding; IEA.		
DR	GO; GO:0006508; P.proteolysis and peptidolysis; IEA.		
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DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hypothetical protein.
FT NON TER
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Best Local Similarity 88.2%; Pred. No. 9.4e-162;
Matches 450; Conservative 15; Mismatches 18; Indels 27; Gaps 1

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DB 61 LELEIQLANTIVPQDQRDEEKIHKMSISELQALAPAVDWLEFLSLFLELSDSEPV 120
QY 409 VTGMDYVQQVSELINRTSEILNNVYLWNLVQKTTSSLDRPFESAQEKILETLYGKKS 468
DB 121 VVTGVEYVQQVSELINRTSEILNNVYLWNLVQKTTSSLDRPFESAQEKILETLYGKKS 180
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QY 589 QLRKPSRDQSMTPQTVNAVYLLPTKNEIVEPAGILOAPFYARHHPKALNFGIGVWGH 648
DB 301 QLRKPSRDQSMTPQTVNAVYLLPTKNEIVEPAGILOAPFYARHHPKALNFGIGVWGH 360
QY 649 ELTAFPDQGEYKKEGTLRPWMQNESLAAIRNTACMEBOYQYVNGGERLNGRQTIGE 708
DB 361 ELTAFPDQGEYKKEGTLRPWMQNESLTAQNTACMEBOYSQYVNGGERLNGRQTIGE 420
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**ORIGIN**

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Db	61	GGGAGCGGGCCAGCTGCCGGAGACCCTGA	ATACCGCCTGGCCGACTCAACATGAACG	120
OY	121	TCGCGCTGCAGAGCTGGAGCTGGCAG	CAACATGCTGAGTGAACAAACGGGCACGCTTC	180
Db	121	TCGCGCTGCAGAGCTGGAGCTGGCAG	CAACATGCTGAGTGAACAAACGGGCACGCTTC	180
OY	181	GGGAGGAAGA	CGCACCCGAGACCCCGTAGAGGGGGGGCCCTCCCGGACCGCAATGAGAG	240
Db	181	GGGAGGAAGA	CGCACCCGAGACCCCGTAGAGGGGGGGCCCTCCCGGACCGCAATGAGAG	240
OY	241	TGGGCAAGGGGGCTTCCCTTTCTCA	CAGAGCGCCAGCGCTTGACATGACGCTTGACAC	300
Db	241	TGGGCAAGGGGGCTTCCCTTTCTCA	CAGAGCGCCAGCGCTTGACATGACGCTTGACAC	300
OY	301	CCAGAGCTCTGGGCTGTTCTGGAGGGTCA	CTGCCCCCACTCCGCTCCATCTTGAGCC	360
Db	301	CCAGAGCTCTGGGCTGTTCTGGAGGGTCA	CTGCCCCCACTCCGCTCCATCTTGAGCC	360
OY	361	TCTGCTCTAGAGCTATGATGGGGA	ATTCCGAAAGGGGACAAGACAGTGTATGAGCTCAACGCA	420
Db	361	TCTGCTCTAGAGCTATGATGGGGA	ATTCCGAAAGGGGACAAGACAGTGTATGAGCTCAACGCA	420
OY	421	CGCAGCTGAGAGCTGGTCTTAGCAGGCTGCCTCTA	CTGCTGGCTCACTGCTTCTGGGCT	480
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OY	481	GCTTTGTG3CCCTAG3GGGTCCAGTA	CCACAGAGCCATCCCAACAGCACTGCTTTAG	540
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Db	601	GTGAGGACTTTTACAGATTCTCTGTGGGGGCTGGA	ATTCCGAGAGAACCCCTGCGCGATG	660
OY	661	G3CGTTCCTGCTGGAACCTTCA	CAGCCTCTG3GACCAAAACGAGCCATCTGAAGC	720
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OY	721	ACCTGCTTGA	AAACACCACTTCAACTCGAGAGTGAAGCTGAGAGAAACACAGCCCT	780
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OY	781	TCTACCTATCTTGCTTACAGGTGGA	CGCATTTGAGAGCTGGAGCCCGAGCCACTGAGAG	840
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OY	841	ACCTCATTTGAGAGATTTGGTGGT	TGGAACATTAAGGGGGCCCTGGAGCCAGGACAACTTTA	900
Db	841	ACCTCATTTGAGAGATTTGGTGGT	TGGAACATTAAGGGGGCCCTGGAGCCAGGACAACTTTA	900
OY	901	TGAGAGTGTGAAGGACGTAGCAGGAC	CTTACAGGGCCACCCCATTTCTTCAACCGTCTACA	960
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QY	961	TCAGTGCACACTCAAGATTCACAACGCAATGTTATCCAGTGTGACCACTTCGGGCTCT	1020
DB	961	TCAGTGCACACTCAAGATTCACAACGCAATGTTATCCAGTGTGACCACTTCGGGCTCT	1020
QY	1021	TTCTGCGCCTCCGGGATTACTACTTAACAAGAACTGGCAATGAGAAAGTCTCACTGCTC	1080
DB	1021	TTCTGCGCCTCCGGGATTACTACTTAACAAGAACTGGCAATGAGAAAGTCTCACTGCTC	1080
QY	1081	ATCTGATTTACATGAGGAACCTGGGGATGCTGCTGGGTGGCGGCCACTTCCAAGAGG	1140
DB	1081	ATCTGATTTACATGAGGAACCTGGGGATGCTGCTGGGTGGCGGCCACTTCCAAGAGG	1140
QY	1141	AGCAGATGACAGCACTGCTGGAGTTGAGATATACAGCTGGGCAACATACAGTGGCCCAAG	1200
DB	1141	AGCAGATGACAGCACTGCTGGAGTTGAGATATACAGCTGGGCAACATACAGTGGCCCAAG	1200
QY	1201	ACCAGCGCGCGACGAGAGAGAAAGATCTACCAACAAGATGAGCAATTCGAGCTGCAGGCTC	1260
DB	1201	ACCAGCGCGCGACGAGAGAGAAAGATCTACCAACAAGATGAGCAATTCGAGCTGCAGGCTC	1260
QY	1261	TGGGGCCCTCCATGGAATCGGCTTGAAGTTCCCTGCTCTTCTTGCTGTCAACAATTGAGATTGA	1320
DB	1261	TGGGGCCCTCCATGGAATCGGCTTGAAGTTCCCTGCTCTTCTTGCTGTCAACAATTGAGATTGA	1320
QY	1321	GTGACTCTGAGCCTGTGTGTGTATGGAATGGAATTTATTGACAGAGGTGTCAAGCTCA	1380
DB	1321	GTGACTCTGAGCCTGTGTGTGTATGGAATGGAATTTATTGACAGAGGTGTCAAGAGCTCA	1380
QY	1381	TCAACCGACGGAACCAAGCATCTGTAAACAATTACTGATCTGGAACCTGTGTCAAAAAGA	1440
DB	1381	TCAACCGACGGAACCAAGCATCTGTAAACAATTACTGATCTGGAACCTGTGTCAAAAAGA	1440
QY	1441	CAACCTCAAGCCTGTGACCGACTTTTGAAGTCTGACAACAAGAAAGCTCTGGAAGCCTCT	1500
DB	1441	CAACCTCAAGCCTGTGACCGACTTTTGAAGTCTGACAACAAGAAAGCTCTGGAAGCCTCT	1500
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DB	1501	ATGGCACTAAGAGTCTGTGTGTGTCGAGGTGGCAGACCTGTGATCTCCAACAACGATGACG	1560
QY	1561	CCCTTGGCTTGTCTTTGGGGGTCCCTCTTCCGTGAAGGCAAGTTTGAACCGGCAAAAGCAAG	1620
DB	1561	CCCTTGGCTTGTCTTTGGGGGTCCCTCTTCCGTGAAGGCAAGTTTGAACCGGCAAAAGCAAG	1620
QY	1621	AAATTTGACAGAGGGGATGATCAGCCAAATCCGGAACCGCATTTGAGAGGCGCCTGGGACAGC	1680
DB	1621	AAATTTGACAGAGGGGATGATCAGCCAAATCCGGAACCGCATTTGAGAGGCGCCTGGGACAGC	1680
QY	1681	TGCTTTGGATGAGATGAGAAAGACCCGCCAGGCAAGCAAGGAGAAAGCAGATGCCATTCATG	1740
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QY	1801	GGTACGAATTTCTGAAGATTCCTTCTTCCAAAACATGTTGAATTTGTACCACTTCTCTG	1860
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QY	1921	CCGACAGAGTGAATGCTACTTACTCTTCCAACCTAAGATGAGATGCTTCCCGCTGGCA	1980
DB	1921	CCGACAGAGTGAATGCTACTTACTCTTCCAACCTAAGATGAGATGCTTCCCGCTGGCA	1980
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DB	1981	TCCTGACAGGCCCCCTTCTATGCCCCGCAACACCCCAAGGCCCTGGAATCTTGGGTGACATCG	2040

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Db	2041	GTGTGTCATATGGGCCCATATGATTTGACGCAATGCTTTGATGACCAAGGGGCGCATATGACA	2100
OY	2101	AAGAAAGGAACTGTGCGGCTCTGTGTGGCAATGATCCCTGGCAAGCTTCCGGAACCA	2160
Db	2101	AAGAAAGGAACTGTGCGGCTCTGTGTGGCAATGATCCCTGGCAAGCTTCCGGAACCA	2160
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Db	2161	CGGCTGTGATGAGAGAACATGTAACAATCAATACCAAGTCAATGGGGAGAGGCTCAACGGCC	2220
OY	2221	GCCAGACGCTATGGGGGAGAACTATGCTGCAACCGGGGGGCTAAGCTCCCTCAATGCTT	2280
Db	2221	GCCAGACGCTATGGGGGAGAACTATGCTGCAACCGGGGGGCTAAGCTCCCTCAATGCTT	2280
OY	2281	ACAAAGCAATGCTGTGAAAGACATGGGGGAGAGACAACTCCACGCGTGGGGCTCAACCA	2340
Db	2281	ACAAAGCAATGCTGTGAAAGACATGGGGGAGAGACAACTCCACGCGTGGGGCTCAACCA	2340
OY	2341	ACCAACAGCTCTTCTTGTGTGGGATTTGCCAGGTGTGCTCGGTCCGACACACAAAGA	2400
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OY	2461	CTCTCTCAACCTCCCGTATCTTCCGTGGGCACTTCGCGTGCCTGTGGGCTCCGCCATGA	2520
Db	2461	CTCTCTCAACCTCCCGTATCTTCCGTGGGCACTTCGCGTGCCTGTGGGCTCCGCCATGA	2520
OY	2521	ACCCAGGGCAGCTGTGTAGGGTGTGTAGACCTGTATCAGGGGAGAAATGCCCCAGCTGTC	2580
Db	2521	ACCCAGGGCAGCTGTGTAGGGTGTGTAGACCTGTATCAGGGGAGAAATGCCCCAGCTGTC	2580
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OY	2761	TTCACTGTGACATCTTTCCTGTGTACCCCTGCTGTGAAAGGCTCTGTGTGGGAGAGCACT	2820
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Db	2881	GCTGTGCGCTGTGCGGCCCATCTGTACCCACAGGCTGGGTGTGTACTCTCTGTGAATTTCT	2940
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AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
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			Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,	
			Nomura,N. and Ohara,O.	
			Prediction of the coding sequences of unidentified human genes. IX.	
			The complete sequences of 100 new cDNA clones from brain which can	
			code for large proteins in vitro	
JOURNAL			DNA Res. 5 (1), 31-39 (1998)	
MEDLINE			98290545	
PUBMED			9628581	
REFERENCE			2 (bases 1 to 3228)	
AUTHORS			Ohara,O., Nagase,T. and Ishikawa,K.	
TITLE			Direct Submission	
JOURNAL			Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute,	
			DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan	
			(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,	
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## ORIGIN

Query Match 88.5%; Score 2988.4; DB 9; Length 3138;  
Best Local Similarity 95.8%; Pred. No. 0;  
Matches 3137; Conservative 0; Mismatches 1; Indels 138; Gaps 1;

QY 66 CGGGCCGAGCTGCGGGGAGCCCTGGAATGACCGCCCTGGCCCGGACTCCACATGAAGAGTGGCG 125  
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QY 246 AAGGGGGCTTCCCTTCTCAACGAGGCCCGCTGGCATGAGCGCTGGGACACCCAGG 305  
DB 174 ----- 173

QY 306 AGCTGGGCTGTTCTGAGAGGATCACTGCCCGCCTCCATCTGAGCTTCG 365  
DB 174 ----- 173

QY 366 TCTAGACATATGTTGGGATTCAGAGAGGGGACAGACGCTTTAGGCTCAAGCAGCAG 425  
DB 174 ----- 173

QY 426 CTGAGAGCTGGCTTAGACAGGAGCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTTCCT 485  
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QY 486 GTGGCCCTAGGGGCTCAGATACACAGAGCCCATCCACAGCAGCTTCCTTACAGAGCC 545  
DB 283 GTGGCCCTAGGGGCTCAGATACACAGAGCCCATCCACAGCAGCTTCCTTACAGAGCC 342

QY 546 TGCATTGAGTGGCTGAGAAATCTCTGAGTCCCTGAGCCGAGGGGAGGCGCCCTGAG 605  
DB 343 TGCATTGAGTGGCTGAGAAATCTCTGAGTCCCTGAGCCGAGGGGAGGCGCCCTGAG 402

QY 606 GACTTTTACAGGTTCTCCTGAGGGGCTGATTCGAGAGAAACCCCTGCGGAGTGGGCT 665  
DB 403 GACTTTTACAGGTTCTCCTGAGGGGCTGATTCGAGAGAAACCCCTGCGGAGTGGGCT 462

QY 666 TCTGCTGAGAACACTTCACAGCCTCTGGAGCCAAACAGGCGCATCTGAAGCAGCTG 725  
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QY 726 CTTGAAAAACACCTTCACTCCAGCAGTGAAGCTGAGAGAAACAGGCGCTTCTAC 785  
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QY 906 GTGTTGAAGAGATGAGAGAGCCTACAGGCGCAACCCCATCTTCAACCTGATACAGT 965  
DB 703 GTGTTGAAGAGATGAGAGAGCCTACAGGCGCAACCCCATCTTCAACCTGATACAGT 762

QY 966 GCCGACTTAAGAGTTTCAAGAGCAATGTTATCCAGTGAAGCAGTGGGCTCTTTCTG 1025  
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QY 1026 CCCTCTGCGGATTAATCTAATTAACGAATGACCAATGAAGAGTGTCACTGCTATCTG 1085  
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QY	2166	TGCATGAGAGAA	CAGTATACATCAATAACAGGCTCAATGGGAGAGAGGCTCAACGGCGCCAG	2225B
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QY	2406	CACGAGGGGCTG	TATGACCAACCCACAGCCCTGCCCCCTTCCGAGTCTAGGGCACTCTC	2465B
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QY	2766	TGTGACATCTT	TCCGATCACCCCTGACCTGTGACAGAGAGTCTGGGTGGGAGGCGCAGTTCCCA	2825B
Db	2563	TGTGACATCTT	TCCGATCACCCCTGATCACCCCTGTCTGTGAAGAGTCTGGGTGGGAGGCGCAGTTCCCA	2622A
QY	2826	TAGGAAGAGT	CTGTGCTTCTGTATCCACAGGCTCACTCAGCCTGACGCGCACATGGGAGCTGT	2885B
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QY	2886	CCGTGCTCGCC	CACTGTGACCCACAGGCTGGGTGTATCTCTGTGAATTCTTCCCA	2945A
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QY	2946	GGCTCACTCAG	TATGGGCACTTAGGGGTGACCTCAGCTGTGTGGCTACCCCTCAACGGGCT	3005B
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QY	3066	TGAAGACTCT	ATGTGGAAGCCCAAGAGGCTCTGTAAAGCTCTCTGTGCCACTGTATTC	3125B
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Db 3443 AGGAGGACACAGCTTTATTTTATACAGAAAAGAGGCTGGAGAGGCTGTGGTCTTGGCCCTTA 3102

Qy 3306 TAGGACCCCTGTGCCAATAAACAGCATGCAATCCGTC 3341

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RESULT 4	AF428263	3410 bp	mRNA	linear	PRI 11-JAN-2002
LOCUS	AF428263				
DEFINITION	Homo sapiens endothelin converting enzyme-2A (ECE2) mRNA, complete cds; alternatively spliced.				
ACCESSION	AF428263				
VERSION	AF428263.1	GI:16903012			

SOURCE ORGANISM	Source Organism
Homo sapiens (human)	Homo sapiens (human)
Homo sapiens	Homo sapiens

REFERENCE 1 (bases 1 to 3410)

TITLE Human endothelin converting enzyme-2 (ECE2) : characterization of

MEDLINE 21575691

**AUTHORS** Lorenzo, M.-N., Khan, R.Y., Wang, Y., Tai, S.C., Chan, G.C., Cheung, A.H.

JOURNAL Submitted (05-OCT-2001) Medicine, University of Toronto, 1 King's

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CDS	255.2618
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deposited in GenBank Accession Number AF192531"

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DOVSELINRTEPSILNNYLINWLVOKTTSSLDRFBSAOEKLLETLYGTKSCVPRWO

AKENADAI I DMIG FDI DEFKEEDV I DGI EISEDS FQNMENLINF SAKVADQ  
RKP SRDOWSMT POTV NAYL PTKNEI VEPAGILOAPFYARNHPKALNFGIGVMGH

GENIADNGGELNCHINAIKAMLRKHGEZQDLFAVGLINHQLFVGFAGVWC3VKLFSS  
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Query Match 87.8%; Score 2964.6; DB 9; Length 3410;

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1511 GAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1570

1580 GAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1639  
1571 TGTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1630  
1640 TGTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1699  
1631 GGGGATGATCAGGAAATCCGAGCCGCACTTGAAGAGGCTGCTGCTGCTGCTGCTGCTGCT 1690  
1700 GGGGATGATCAGGAAATCCGAGCCGCACTTGAAGAGGCTGCTGCTGCTGCTGCTGCTGCT 1759  
1691 GATGAGAAAGACCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1750  
1760 GATGAGAAAGACCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819  
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1811 TTTCCAGACTTATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1870  
1880 TTTCCAGACTTATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939  
1871 GCTGACCAAGCTTCCGAGGCTTCCGAGCCGAGCAAGTGAAGATGACCCCGACAGCT 1930  
1940 GCTGACCAAGCTTCCGAGGCTTCCGAGCCGAGCAAGTGAAGATGACCCCGACAGCT 1999  
1931 GAATGCTTACTTACTTCTTCACTTGAAGATGAGATGCTTCCGCTGCTGCTGCTGCTGCT 1990  
2000 GAATGCTTACTTACTTCTTCACTTGAAGATGAGATGCTTCCGCTGCTGCTGCTGCTGCT 2059  
1991 CCCCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2050  
2060 CCCCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2119  
2051 GGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2110  
2120 GGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2179  
2111 CTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2170  
2180 CTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2239  
2171 GAGAGAAAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2230  
2240 GAGAGAAAGTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2299  
2231 GGGGAGAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2290  
2300 GGGGAGAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2359  
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2360 GCTGAGAAAGCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2419  
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2420 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2479  
2411 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2470  
2480 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2539  
2471 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2530  
2540 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2599  
2531 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2590  
2600 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2659  
2591 GGGGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2650

Db	2660	GGGCGACGTCTCCTGCAAAAGCGTTTGCCTTGGTTGGAGGAAGCAAAATGCAAGCTGG	2711
Qy	2651	GCTGGGCTTAAGTCCCTCCCCCCCAAGGTGACATGATGACAGACCTTCTCTAATACAC	2710
Db	2720	GCTGGGCTTAAGTCCCTCCCCCCCAAGGTGACATGATGACAGACCTTCTCTAATACAC	2779
Qy	2711	ATTGGGCTCTGCTTTTGGGGGGGCGCCCTGCCACAGAGAGGCGCCCACTTCACTGGGA	2770
Db	2780	ATTGGGCTCTGCTTTTGGGGGGGCGCCCTGCCACAGAGAGGCGCCCACTTCACTGGGA	2835
Qy	2771	CATCTTTCCTGTCACCCCTGCCTGGAAAGGCTCTGGTGGGGAGGCGAGTTTCCATAGA	2830
Db	2840	CATCTTTCCTGTCACCCCTGCCTGGAAAGGCTCTGGTGGGGAGGCGAGTTTCCATAGA	2895
Qy	2831	AGAGGTCTGCTCTTCTGTCTGCCAGGCTCACTCAGCTCGGCGGCATGCGGCTGCGGTG	2890
Db	2900	AGAGGTCTGCTCTTCTGTCTGCCAGGCTCACTCAGCTCGGCGGCATGCGGCTGCGGTG	2955
Qy	2891	CCTGCGCCACATGTGACCCCAAGGCGCTGGGTGGTGTAACTTCTGTGACCTTCTCCAGGCTC	2950
Db	2960	CCTGCGCCACATGTGACCCCAAGGCGCTGGGTGGTGTAACTTCTGTGACCTTCTCCAGGCTC	3015
Qy	2951	ACTCAGTGCAGCACTTAAGGGGTGGACTCAGCTCTGTGGATCACTCAGCGGCTAACCC	3010
Db	3020	ACTCAGTGCAGCACTTAAGGGGTGGACTCAGCTCTGTGGATCACTCAGCGGCTAACCC	3075
Qy	3011	CACCTCAACCTGTGCTCTTGTGCCACATGCTCCAGTCTGTGCTGACCTTCACTGACA	3070
Db	3080	CACCTCAACCTGTGCTCTTGTGCCACATGCTCCAGTCTGTGCTGACCTTCACTGACA	3135
Qy	3071	GCTCCTTAATGGAAAGCCCAAGGGCTCTGTAAAGCTCTGTGCTGCCACTGTCTTCTGGGC	3130
Db	3140	GCTCCTTAATGGAAAGCCCAAGGGCTCTGTAAAGCTCTGTGCTGCCACTGTCTTCTGGGC	3195
Qy	3131	TGAGAGGGGAAGTGCAATATGTGTAGCGGGTACTGGTCTGTGTCTTAAGGGCAAAAGCT	3190
Db	3200	TGAGAGGGGAAGTGCAATATGTGTAGCGGGTACTGGTCTGTGTCTTAAGGGCAAAAGCT	3255
Qy	3191	TAGCAAAATGATTAATTTCTCCCTGCACAAAGCAGAAACAGATAGACAGGGAAAGAA	3250
Db	3260	TAGCAAAATGATTAATTTCTCCCTGCACAAAGCAGAAACAGATAGACAGGGAAAGAA	3315
Qy	3251	GAAACAGATTAATTTTTCAGAAAAGAGGGTGGAGGGTGTGTCTTGGCCCTTATAGGA	3310
Db	3320	GAAACAGATTAATTTTTCAGAAAAGAGGGTGGAGGGTGTGTCTTGGCCCTTATAGGA	3375
Qy	3311	CCCTGTGCCAATPAAACAGACATGCATCCGTC	3341
Db	3380	CCCTGTGCCAATPAAACAGACATGCATCCGTC	3410
RESULT 5	AF428264		
LOCUS	AF428264	3051 bp	mRNA linear PRI 11-JAN-2002
DEFINITION	Homio sapiens endothelin converting enzyme-2B (ECE2) mRNA, complete cde; alternatively spliced.		
ACCESSION	AF428264		
VERSION	AF428264.1	GI:16903014	
KEYWORDS			
SOURCE	Homio sapiens (human)		
ORGANISM	Homio sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Lorenzo,M.N., Khan,R.Y., Wang,Y., Tai,S.C., Chan,G.C., Cheung,A.H. and Marsden,P.A.		
TITLE	Human endothelin converting enzyme-2 (ECE2): characterization of mRNA species and chromosomal localization		
JOURNAL	Biochim. Biophys. Acta 1522 (1), 46-52 (2001)		
MEDLINE	21575691		
PUBMED	11718899		
REFERENCE	2 (bases 1 to 3051)		
AUTHORS	Lorenzo,M.-N., Khan,R.Y., Wang,Y., Tai,S.C., Chan,G.C., Cheung,A.H.		

FEATURES	source
gene	<p>1. .3051</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>1. .3051</p> <p>/gene="ECE2"</p> <p>49. .2259</p> <p>/gene="ECE2"</p> <p>/note="ECE-2B; alternatively spliced form of isoform ECE-2B deposited in Genbank Accession Number AF192531"</p> <p>/codon_start=1</p> <p>/product="endothelin converting enzyme-2B"</p> <p>/protein_id="A130387.1"</p> <p>/db_xref="GI:16903015"</p> <p>/translation="MNVALDELGAGSVNGFQKTRQLSGRTQLELYLAASLLIALLLDCLVALGVQYHRDPSHSTCLTEACIRVAGKLLSELDKRVSPEDYQSGCGMIRNPLPDGRSMNTNPSLMDQNALILKHLNNTTNSSEAEAKTORFYLSCLOVERIEELGAPFLADLLEKIGAMNITGPMODNMETVLKAVGRTAFPTVYISADSKSNLSVIODOSGLFLPRDYLANRITANEKUTALDYMEELGAMLPGRPTSTREMOVELLEIQLANTVPODQRDEBEKTYHKGISSELDALAPSNMNEFLSTLSPILSSEPPVYVGDYLDQVYSINLTREPSILNNYLIMNLVQKTSLSLDRFESAOGLLETLTGKKSCEPRWOTCISLNTDRLQAFALGSLFVYATPRDQSKELAEOMISEIRAFEBALGQLVWMEKTRQAKAEKADALYDMIGPDPFLPEKELDVGVEISDFSPNNKALYNFSAKMAADOLRAKEPESDOMSMTQPTVNAAYLLPKNEILVPAGLILQAPFAPRNPKALFGSGALVGMGHELTTHAPDQGRKYDKXGNLRPMQNSLSLAFRHHTHCMEOVNOYNGERLNGRQITGENIADNGELKALYNAKMYKMLRKHGEQQLPAYGLTRHQLFPFGQVQWCSVRTPESHBEGLVTDPHSPARFVRLGTLNLRDPLRHRCFVSPMNPGLCEW"</p>
CDS	
Query Match	87.8%; Score 2964.4; DB 9; Length 3051;
Best Local Similarity	99.6%; Pred. No. 0; Mismatches 11; Gaps 0;
Matches 2971; Conservative	0; Indels 0; Gaps 0;
Db	360 CTCTGCTCTAGGACTATGATGAGGATTCAGAGGGGCAAGACAGCTGTAGGCTCA 419
Db	70 CTGGAGCTGGGAGCAACGTGGGATTCAGAGGGGCAAGACAGCTGTAGGCTCA 129
Qy	420 ACGCAGCTGAGAGCTGTCTTAGCAGGTCCTCTTACTGTGCTGGTGAATGCTTCTG 479
Db	130 ACGCAGCTGAGAGCTGTCTTAGCAGGTCCTCTTACTGTGCTGGTGAATGCTTCTG 189
Qy	480 TGCCTTGTGGCCCTAGGGGTCAGTACCAAGAGACCCATCCACACAGCATCTTACA 539
Db	190 TGCCTTGTGGCCCTAGGGGTCAGTACCAAGAGACCCATCCACACACAGCATCTTACA 249
Qy	540 GAGGCTGCAATCGAGTGTGCTGGAATAATCTGTGAGTCCCTGGAACGAGGGGTGAG 599
Db	250 GAGGCTGCAATCGAGTGTGCTGGAATAATCTGTGAGTCCCTGGAACGAGGGGTGAG 309
Qy	600 TGTGAGGACTTTTACAGTTCTCCTGTGAGGCTGATTCGAGAGAACCCCTGCGCAT 659
Db	310 TGTGAGGACTTTTACAGTTCTCCTGTGAGGCTGATTCGAGAGAACCCCTGCGCAT 369
Qy	660 GGGGTTCTGCTGGAACACCTTCAACAGCTCTTGGGACCAAAACCAAGGCTATCTGA 719
Db	370 GGGGTTCTGCTGGAACACCTTCAACAGCTCTTGGGACCAAAACCAAGGCTATCTGA 429
Qy	720 CACCTGTTGAAAACACCTTCAACTCCAGCAGTGAACCTGAGCAGAGACACACAGCG 779
Db	430 CACCTGTTGAAAACACCTTCAACTCCAGCAGTGAACCTGAGCAGAGACACACAGCG 489
Qy	780 TTCTACCTATCTTGCTTACAGGTGAGCGGATTTGAGGAGCTGGGAGCCCAAGCATG 839
Db	490 TTCTACCTATCTTGCTTACAGGTGAGCGGATTTGAGGAGCTGGGAGCCCAAGCATG 549
Qy	840 GACCTCATTTGAGAGATTTGGTGTGGAACATTACGGGGCCCTGGGACCAAGCAATTT 899
Db	550 GACCTCATTTGAGAGATTTGGTGTGGAACATTACGGGGCCCTGGGACCAAGCAATTT 609

QY 900 ATGAGGTGTTGAAGGAGTACGAGGAGCCTACAGGGGCCAACCCTTCTTCAACGCTCTAC 959  
DB 610 ATGAGAGTGTGGAAGGAGTACGAGGAGCCTACAGGGGCCAACCCTTCTTCAACGCTCTAC 669  
QY 960 ATCAGTCCGCACTCTAAGAGTTTCCAGCAGCAATGTTATCCAGGTGAGCAAGTCTGGCTC 1019  
DB 670 ATCAGTCTGAATCTTAAGAGTTTCCAGCAGCAATGTTATCCAGGTGAGCAAGTCTGGCTC 729  
QY 1020 TTTCTGCTCTCTGGGATTAATACTTAACAGAACTGCCAATGAGAAAGTCTCACTGCC 1079  
DB 730 TTTCTGCTCTCTGGGATTAATACTTAACAGAACTGCCAATGAGAAAGTCTCACTGCC 789  
QY 1080 TATCTGATTAATCAATGAGGAACTGGGGATGCTGCTGGGGGGGGGGGGGGGGGGGGGGGG 1139  
DB 790 TATCTGATTAATCAATGAGGAACTGGGGATGCTGCTGGGGGGGGGGGGGGGGGGGGGGGG 849  
QY 1140 GAGCAGATGAGCAGAGTGTCTGAGTGAAGTACAGCTGGCCAACTACAGTGGCCAG 1199  
DB 850 GAGCAGATGAGCAGAGTGTCTGAGTGAAGTACAGCTGGCCAACTACAGTGGCCAG 909  
QY 1200 GACCAAGCGGCGGCGAGCAGAGAGAGATCTACCAAGATGAGCAATTTGGAGCTGAGGCT 1259  
DB 910 GACCAAGCGGCGGCGAGCAGAGAGAGATCTACCAAGATGAGCAATTTGGAGCTGAGGCT 969  
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DB 970 CTGGCGGCTCTCCAGTGAAGTGGCTGAGTCTGCTTCTTCTGCTGCAACATTTGAGTGG 1029  
QY 1320 AGTGACTCTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379  
DB 1030 AGTGACTCTGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1089  
QY 1380 ATCAACCGCAGCGAACCAGAGATCTTGAACATTAATCTGATCTGGAACCTGGTGGAAAG 1439  
DB 1090 ATCAACCGCAGCGAACCAGAGATCTTGAACATTAATCTGATCTGGAACCTGGTGGAAAG 1149  
QY 1440 ACAACCTCAAGCTCGAGCCGAGCGCTTGAAGTCTGCAAGAGAGAGCTGGAGAACCTC 1499  
DB 1150 ACAACCTCAAGCTCGAGCCGAGCGCTTGAAGTCTGCAAGAGAGAGCTGGAGAACCTC 1209  
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DB 1210 TATGCACTAAGAGTCTGTGTGCGAGAGTGGCAGACCTGCATCTCCAAACCGGATGAC 1269  
QY 1560 GCCCTTGGCTTGTCTTGGGGTCCCTCTTGTGAAGGCGACGTTTGAACCGCAAGCAAA 1619  
DB 1270 GCCCTTGGCTTGTCTTGGGGTCCCTCTTGTGAAGGCGACGTTTGAACCGCAAGCAAA 1329  
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DB 1510 GGGATGAGAAATTTCTGAAGATTTCTTCTTCCAAAGATGTTGATTTGTTCAACTTCTCTCT 1569  
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QY 2040 GGTGTGATCAATGAGGAGATGATGAGCAGATGCTTGTATGATCAAGAGGCGGAGATGATGAC 2099  
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Db 1202 GCCCTTGCTTTGGGCTCCCTCTGTCGTAAGGCAAGCTTTGACCCGCAAAAGCAA 1261  
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Db 1262 GAAATTGCAAGGGGATGATTCAGGAAATCCGGAACCCGCTTTGAGAGGCCCTGGGACAG 1321  
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Db 1442 GGGTACGAAATTTCTGAAAGATTTCTTCTCCAAAAGATTTGAAATTTGTACAATTTCT 1501  
Qy 1860 GCCAAGGTTATGCTGACAGCTCCGCAAGGCTCCGACGCAAGAGCAAGTGAAGATGAC 1919  
Db 1502 GCCAAGGTTATGCTGACAGCTCCGCAAGGCTCCGACGCAAGAGCAAGTGAAGATGAC 1561  
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Db 2642 CCGGCTTACCCCACTCACTGTCCTTCTGTCGTCCTTCCAGTGTGTCGTCGAC 2701  
Qy 3060 CTTCACTGACAGCTCTTCAAGGAGCCCAAGGCTCTGAAAGCTCTGCTGCGCACTG 3119  
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Db 2762 TTTCCCTGGCTGAGAGGAGGAAATGATGATGATGATGATGATGATGATGATGATG 2821  
Qy 3180 GGCACAAAGC-TTAGCAATATGATTTGATTTCTCCCTGACCAAGAGAGAAAGCATGAGC 3238  
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Db 2942 GCCCTTATAGACCTGTGTCATTAACAGACATGATCTGTCATTAACAAAAA 3000

RESULT 7  
AF521189 2667 bp mRNA 1linear PRI 15-JUL-2002  
LOCUS  
DEFINITION  
Homo sapiens endothelin-converting enzyme-2C (ECE2) mRNA, complete cds.  
ACCESSION  
AF521189  
VERSION  
AF521189.1 GI:21780270  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 2667)  
Funke-Kaiser, H., Scheuch, K., Behrouzi, T., Synowitz, M., Draheim, N., Schwaneberg, B., Thomas, A., Zollmann, F. S., Paul, M., and Orzechowski, H. D.  
Human endothelin-converting enzyme-2C (ECE-2C): a new ECE-2 variant  
TITLE  
Unpublished  
JOURNAL  
2 (bases 1 to 2667)  
Funke-Kaiser, H., Scheuch, K., Behrouzi, T., Synowitz, M., Draheim, N., Schwaneberg, B., Thomas, A., Zollmann, F. S., Paul, M., and Orzechowski, H. D.  
Direct Submission  
JOURNAL  
Submitted (13-JUN-2002) Clinical Pharmacology and Toxicology, Benjamin Franklin Medical Center, Freie Universitat Berlin, Hindenburgdamm 30, Berlin 12200, Germany  
FEATURES  
Location/Qualifiers





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AX376352  
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DEFINITION Sequence 419 from Patent WO0168848.  
ACCESSION AX376352  
VERSION AX376352.1 GI:19170567  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,  
Guiney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0168848-A 419 20-SEP-2001;  
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QY 420 AGGAGCTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 479  
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QY 540 GAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599  
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QY 840 GACCTCATGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 899  
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QY 900 ATGAGAGTTTGAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 959  
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 ACCESSION AY359003  
 VERSION AY359003.1 GI:37183123  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2602)  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,O., Hass,P.B.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,B., Sanchez,C.,  
 Schenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vegte,A., Vandlen,R., Watanabe,C., Wiendel,D., Woods,K.,  
 Xie,M.H., Yanzura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
JOURNAL A Bioinformatics Assessment  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 2602)  
AUTHORS Clark H.P.  
TITLE Direct Submission  
JOURNAL Submitted (01-NOV-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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QY 2160 ACGGCTGCAATGAGGAAAGATCAATCAATACCAAGTCAATGAGGAGAGGCTCAACGGC 2219  
Db 1921 ACGGCTGCAATGAGGAAAGATCAATCAATACCAAGTCAATGAGGAGAGGCTCAACGGC 1980  
QY 2220 CCGCAGACGCTGAGGAGAAATTTGCTGACACGAGGAGGCTGAAAGCTGCTCAATGCT 2279  
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QY 2340 AACCAACAGCTTCTTCTGAGGAAATTTGAGGAGTGTGCTCGGCTCGGCAACAGAG 2399  
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Db 2161 AGCTCTCAGAGGAGGCTGTGACCGAACCCCAAGCCCTGCGCTTCCGCTGCTGGC 2220  
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Db 2341 CACCAAGCTGAGGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2400  
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QY 2700 TCAATACCAATGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2759  
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Db 2521 ATTCACTGTGACATCTTTCCTGTGTCACTGCTGTGAGAGAGTGTGAGTGTGAGTGTG 2580  
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RESULT 10  
AX100901 2652 bp DNA linear PART 10-APR-2001  
LOCUS AX100901  
DEFINITION Sequence 3 from Patent WO0121773.  
ACCESSION AX100901  
VERSION AX100901.1 GI:13619795

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G.B., Zambrowicz, B. and Sands, A.T.  
TITLE Human endothelein converting enzyme-like proteins and polynucleotides encoding the same  
JOURNAL Patent: WO 0121773-A 3 29-MAR-2001;  
FEATURES Lexicon Genetics Incorporated (US)  
source location/Qualifiers  
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## ORIGIN

Query Match 64.3%; Score 2172.6; DB 6; Length 2652;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2175; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 371 GACTATGCTGAGATTCAGAGGAGGAGCAAGACAGCTGTAGGCTCAAGCAGAGCTGGA 430  
Db 474 GAGTGAAGTGTGAGATTCAGAGGAGGAGCAAGACAGCTGTAGGCTCAAGCAGAGCTGGA 533  
QY 431 GCTGTCTTACAGAGGCTCTTACTGCTGTGCTGCACTGCTTGTGGCTGCTTGTGC 490  
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QY 731 AAACACCACTTCAAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 790  
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QY 911 GAAAGTTGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 970  
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Qy 1451 CTTGAGACCGACGCTTTGAGTCTGCAACAAGAGCTGCTGGAACCTCTATGAGCACTAA 1510  
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Qy 1511 GAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1570  
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Qy 1811 TTTCTGAAAGATTTCTTTCTTCCAAAACATGTTGAATTTGTACAATTTCTCTGCAAGGTTAT 1870  
Db 1914 TTTCTGAAAGATTTCTTTCTTCCAAAACATGTTGAATTTGTACAATTTCTCTGCAAGGTTAT 1973  
Qy 1871 GGGTGAACAGCTCCGCAAGGCTCCGACGAGACCAATGAGCATGACCCCGACAGAGT 1930  
Db 1974 GGGTGAACAGCTCCGCAAGGCTCCGACGAGACCAATGAGCATGACCCCGACAGAGT 2033  
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Db 2094 CCCCCCTTATGCTCCGCAACCAAGGCTGGAATTTGGTGGCATTCGGTGTGCTCAT 2153  
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Qy 2111 CTTGCGGCTCTGTGTGAGATGAGTCTCTGAGCTTCCGGAACCAACGAGCTGCTCAT 2170  
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RESULT 11  
AX360065  
LOCUS AX360065 2298 bp DNA linear PART 13-FEB-2002  
DEFINITION Sequence 21 from Patent WO0200860.  
ACCESSION AX360065  
VERSION AX360065.1 GI:18675691  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Plowman, G., Whyte, D., Sudarshanam, S., Manning, G., Caenepeel, S. and Charyczak, G.  
TITLE Novel proteases  
JOURNAL Patent: WO 0200860-A 21 03-JAN-2002;  
Sugen, Inc. (US)  
FEATURES  
source 1..2298  
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ORIGIN  
Query Match 64.3%; Score 2171.4; DB 6; Length 2298;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 377 GGTGGATTTCCAGAGGGGCAAGAGAGCTGTTAGGCTCAACGACGACGCTGAGTGTGT 436  
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Qy 437 CTTAGCAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 496  
Db 186 CTTAGCAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245  
Qy 497 GGTCAAGTACCAAGAGACCCATCCACAGACCTGCTTACAGAGGCTGACATTTGAGT 556  
Db 246 GGTCAAGTACCAAGAGACCCATCCACAGACCTGCTTACAGAGGCTGACATTTGAGT 305  
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DB 426 CACCTTCAAGAGCTTGGAGCCAAACAGGCCATCTAGAGCACTGCTTGAACAC 485  
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QY 977 GAGTTCACAGCAATTTATCCAGGTGAGCAAGTCTGGGCTCTTTCTGCCCTTCCGGA 1036  
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DB 1026 CTGGCTTGAATCTCTGCTTCTTCTGCTGCAATGAGAGTGGAGTCTGAGAGCTGT 1085  
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DB 1146 AAGCATCTGGAATTAATCTGATCTGGAACCTGCTGCAAAAGCAACCTCAAGAGCTGGA 1205  
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QY 2057 TGAATTTGAGAGATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATG 2116  
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QY 2117 GCCCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2176  
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QY 2417 GGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2476  
DB 2166 GGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2225  
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QY 2537 TGAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2596  
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RESULT 12  
AF489573  
LOCUS AF489573 3291 bp mRNA linear MAM 22-MAR-2003  
DEFINITION Bos taurus endoethelin-converting enzyme 2a-1 mRNA, complete cds.  
ACCESSION AF489573  
VERSION AF489573.1 GI:29150239  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE  
1 (bases 1 to 3291)  
AUTHORS Ikeda,S., Emoto,N., Ikeda,K., Yokoyama,M. and Matsuo,M.  
TITLE Bovine BCE-2a-1  
JOURNAL Unpublished







polya\_signal  
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ORIGIN

Query Match 64.2%; Score 2169.6; DB 4; Length 3291;  
Best Local Similarity 85.3%; Pred. No. 0;  
Matches 2560; Conservative 0; Mismatches 404; Indels 38; Gaps 11;

372 ACTATGAGGATTCAGAGAGGAGCAAGACGCTGTTAGGCTACCGACGACAGCTGAG 431  
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912 AAGCAGTAGCAGGACCTACAGGGGCAACCCATTCTTCAAGCTCATCATGAGTGGAC 971  
842 AAGCAGTAGCAGGACCTACAGGGGCAACCCATTCTTCAAGCTCATCATGAGTGGAC 901  
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1562 GGGATGATCAAGCAAAATCCGGAACCGCATTTGAGAGAGCCCTGAGAGCACTGTTGAGATG 1621  
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1872 GCTGACAGAGTCCGCAAGGCTCCCAAGCCAGAGACAGTGTGAGTACATCCCGGAGAGT 1931  
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1932 AATGCTACTACCTTCAACTCAAGATGAGATGATGATGATGATGATGATGATGATGAT 1991  
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2172 GAGAGCAATGATCAATCAATCAAGTCAATGAGGAGAGGCTCAACGAGGCGGAGAGCTG 2231  
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Db	2342	GGGCTGTGTGAACCGAAGCCCAACAGCCCTCCCGCTTCGCGTGTGTGGGCACTCTCTCCAA	2401
OY	2472	TCCCGTGAAGCTTCCTGTGGGCACTTCGGGCTGCCCTGTGGGCTCCCGCATGAACCCAGGAG	2531
Db	2402	TCCCGTGAAGCTTCCTGTGGGCACTTCGGGCTGCCCTGTGGGCTCCCGCATGAACCCAGGAG	2461
OY	2532	CTGTGTGAAGTGTGTGTGAACCTGTGATCAGGGAGGAATATGCCAGCT---GTCAACAGCC	2588
Db	2462	CTTGTGTGAAGTGTGTGTGAACCTGTGAGTGTGGAGAAATGGCCAGCTCGGTTGCCAGACC	2521
OY	2589	TGGGGCAAGCTCCCGAACAAGCTGTGTGCTTGGGTTGGAGGAAACCAATGCAAGCT	2648
Db	2522	TGGGGTATCTTGTCCACGACAGGCTCTCTGTCTGTGGGTTGATGGAAGGCAATGTCACT	2581
OY	2649	GGGCTGGGTATGATCCCTCCCGCCCAAG--GTGACATGAGTAC-AGAAGCTCCCATC	2705
Db	2582	GGGCTGTGTCTCGGCCCTCCACACATGAGTGTGAACGATGCTATGCTCTCTCGTGGCC	2641
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Db	2702	TGTGA---TGTTCTTTGGCAACCTGTGCTGTGAGAGAGGCTGGGCAAGGCGCACAGCTCC	2758
OY	2825	ATAGAGAGAGTGTGACCTTTCTGTGCCAGGCTCACTCAGCTGGCGCCATGTGGGCT	2884
Db	2759	ACAAGAGAGGGTCCACTCTTTAGAGTCCCAAGCTAGTGGTTGTGTGGCCACAGGGCT	2818
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OY	3064	ACTGAC-----AGCTCTCATGTGGAAGCCCAAGGCGCTTGAAGCTCTCT	3108
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OY	3109	GCT--GCCCATGTGTTTCCCTGGGCTGAGAGAGGGAAGTGCATATGTGTAGCGGATATGGT	3166
Db	3050	TGTTGTGCTCCCAAGGCTCTCTGGGCTCAGCGGGAGTGTGTATCATGTCAAGGAGATGTAGG	3109
OY	3167	TCTGTGTCTTAAAGGC-ACAAGCTTACAAATGATGATTTCTCCCTGTGACAAAGCAGGA	3225
Db	3110	CCCTGTGATCTTGGGGTTTACAAGATCTTAAAGGGGTGTGATCTCTCCGTGACAAGCAGGA	3169
OY	3226	AAGCAGATAGAGCAGGGAAGAAAGAAACAAGTATTTATTTTACAGAAAGAGGTGGGA	3285
Db	3170	AAGCAGATAGAGTGAAGAGAGTGAAGATTAAGTCTATTTTACAGGAAAGGTGAAGGGG	3229
OY	3286	GGGTGTGTCTTGGCCCTTATAGAACCTGTGTGCATTAACAGACATGATCTCGTCAAA	3345
Db	3230	AGGAGTGTGTGGGCCCTGTGAGGACCTGTGTCCAAATAAATAGACAGCATCATGTCAAA	3289
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Db	3290	AA 3291	

RESULT 1.  
AR000480

LOCUS	AR000480	3291 bp	DNA	Linear	PAT 04-DEC-1998
DEFINITION	Sequence 1 from patent US 5736376.				
ACCESSION	AR000480				
VERSION	AR000480.1	GI:3963011			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3291)				
AUTHORS	Yanagisawa, M.				
TITLE	Recombinant endothelin converting enzyme-2 and its use in BCE inhibitor screening				
JOURNAL	Patent: US 5736376-A 1 07-APR-1998;				
FEATURES	Location/Qualifiers				
Source	1..3291				
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Query Match	64.2%;	Score 2169.6;	DB 6;	Length 3291;	
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Qy	432	CTGGTCTTAGCAGGCTGCTCTCTACTGCTG	CTGCACATGCTTCTTGGGCTGTGGCC	491	
Db	362	CTGGTCTTGGCTGGGTGTCTCTACTGTGGCT	CTCCCTTGCGTCTTGGGTGTGGCC	421	
Qy	492	CTAGGGGCTCAGTACACAGAGACCATCCAC	AGCAGCTGCTTTACAGAGGCTGCATT	551	
Db	422	CTGGGGGCTCAGTACACAGAGACCATCCAT	AGCAGCTTGCACAGAGGCTGCATT	481	
Qy	552	CGAGTGGCTGGAAAAATCTCGAGTCCCTGGA	CCGAGGGGAGACCCCTGTGAAGACTTT	611	
Db	482	CGAGTGGCTGGAAAAATCTCGAGTCCCTGGA	CCGAGGGGAGACCCCTGTGAAGACTTC	541	
Qy	612	TACCAGTTCCTCTGGGGGCTGGATT	CGAGAGAACCCCTTGCCGATGGGCTTTCGC	671	
Db	542	TATCAGTTCTCTCGAGAGCTGATTCGAGAA	ACCCTTCACTGATGGGCTTTCGC	601	
Qy	672	TGGAACACTTTCACACAGCCTCTGGGAC	CAAAACGAGGCATATCGAAGCACTTGGAA	731	
Db	602	TGGAACAACTTCACACAGTCTCTGGGAC	CAAGATCAAGGCATCTGAAGCACTTGGAA	661	
Qy	732	AACACCACTTTCACCTCAGAGAGTGAAG	CTGAGCAGAAAGACAGCGCTTTTACTTATCT	791	
Db	662	AACACCACTTTCACCTCAGAGAGTGAAG	CTGAAAGGAAAGCAGCGCTTTTACTCTCC	721	
Qy	792	TGCTACAGGTGGAGCGCATTTAGAGAG	CTGGAGCCCAAGCACTGAGAGACTTCATTGAG	851	
Db	722	TGCTTACAGGTGGAGCGCATGAGAGTGG	GTGGTCCCAAGCACTGAGAGACTTCATTGAG	781	
Qy	852	AAGATTGTGTGGAA	CATTACGGGAGCCCTGGAGCAGAGCA	911	
Db	782	AAGATTGTGTGGCTGGAAGTTACGGGAG	CCCTGGAGCAGAGCACTTCATGGAAGTGTG	841	
Qy	912	AAGCAGTAGCAGGGACCTTACAGGGG	CCACCCCATTTTACCGGTTCATCATGTGCGAG	971	
Db	842	AAGCAGTAGGAGGAGGTATAGGGCC	ACCCCTTCTTACTGTCTAAGTACAGGCCAG	901	
Qy	972	TCTAAGATTCCAAACAGCAATGTATAC	AGGTGGAGCAAGTCTGGGCTCTTTCGCGCT	1031	
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Db	962	CGAATTAATTAATTAACAGGACCG	CAAGTGAAGAAAGTGTCTTACTGTCTTATCGAATTAC	1021	
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RESULT 15  
AF489576  
LOCUS AF489576 3171 bp mRNA linear MAM 22-MAR-2003  
DEFINITION Bos taurus endothelin-converting enzyme 2b-2 mRNA, complete cds.  
ACCESSION AF489576  
VERSION AF489576.1 GI:29150245  
KEYWORDS  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 3171)  
Ikeda, S., Emoto, N., Aikawa, J., Ikeda, K., Yokoyama, M. and  
Matsuo, M.  
TITLE Bovine ECE-2b-2  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 3171)  
Ikeda, S., Emoto, N., Aikawa, J., Ikeda, K., Yokoyama, M. and  
Matsuo, M.  
TITLE Direct Submission  
JOURNAL Submitted (01-MAR-2002) Division of Molecular Medicine,  
International Center for Medical Research, Kobe University Graduate  
School of Medicine, 7-5-1, Kusunoki, Chuo, Kobe 6500017, Japan  
FEATURES  
Source Location/Qualifiers  
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QY 1337 GGTGCTGATGAGATGATTTATTTGAGAGAGTGTAGAGCTCATTAACCGGACCAAGCT 1396  
|||  
Db 1147 GGTGCTGATGAGATGATTTATTTGAGAGAGTGTAGAGCTCATTAACCGGACCAAGCT 1206  
|||  
QY 1397 AAGCATCTGAGCAATTTACCTGATCTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456  
|||  
Db 1207 AAGCATCTGAGCAATTTACCTGATCTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1266  
|||  
QY 1457 CCGAGCTTGTGAGTGTGCAAGAGAGAGCTGCTGAGACCTCTTATGAGCACTTAAGAGTCT 1516  
|||  
Db 1267 CCGAGCTTGTGAGTGTGCAAGAGAGAGCTGCTGAGACCTCTTATGAGCACTTAAGAGTCT 1326  
|||  
QY 1517 CTGTGCTGAGAGTGTGCAAGAGAGAGCTGCTGAGACCTCTTATGAGCACTTAAGAGTCT 1576  
|||  
Db 1327 CTGTGCTGAGAGTGTGCAAGAGAGAGCTGCTGAGACCTCTTATGAGCACTTAAGAGTCT 1386  
|||  
QY 1577 GGGGTCTCTCTTCTGTAAGAGGCAAGTTTGAACGGCAAGCAAGAAATTTGAGAGGGGAT 1636  
|||





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 20:09:01 ; Search time 73 Seconds  
(without alignments)  
3458.235 Million cell updates/sec

Title: US-10-681-222-2

Perfect score: 4281

Sequence: 1 MNVALGELGAGSNMVEYKRA.....RHRCFVSGSPMNGQLCEVW 811

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCP\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
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16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4281	100.0	811	12	US-10-267-502-253
2	4281	100.0	811	14	US-10-273-992-2
3	3993	93.3	765	9	US-09-888-615-80
4	3993	93.3	765	14	US-10-273-992-4
5	3993	93.3	765	15	US-10-453-764-2
6	3824.5	89.3	736	9	US-09-978-2954-526
7	3824.5	89.3	736	9	US-09-978-697-526
8	3824.5	89.3	736	9	US-09-978-192A-526
9	3824.5	89.3	736	9	US-09-999-832A-526
10	3824.5	89.3	736	10	US-09-978-189-526
11	3824.5	89.3	736	10	US-09-978-608A-526
12	3824.5	89.3	736	10	US-09-978-585A-526
13	3824.5	89.3	736	10	US-09-978-191A-526
14	3824.5	89.3	736	10	US-09-978-403A-526
15	3824.5	89.3	736	10	US-09-978-564A-526

16	3824.5	89.3	736	10	US-09-999-833A-526	Sequence 526, App
17	3824.5	89.3	736	10	US-09-981-915A-526	Sequence 526, App
18	3824.5	89.3	736	10	US-09-978-824-526	Sequence 526, App
19	3824.5	89.3	736	10	US-09-918-585A-526	Sequence 526, App
20	3824.5	89.3	736	10	US-09-978-423A-526	Sequence 526, App
21	3824.5	89.3	736	10	US-09-978-193A-526	Sequence 526, App
22	3824.5	89.3	736	10	US-09-999-830A-526	Sequence 526, App
23	3824.5	89.3	736	10	US-09-978-757A-526	Sequence 526, App
24	3824.5	89.3	736	10	US-09-978-187B-526	Sequence 526, App
25	3824.5	89.3	736	10	US-09-978-643A-526	Sequence 526, App
26	3824.5	89.3	736	10	US-09-978-375A-526	Sequence 526, App
27	3824.5	89.3	736	10	US-09-978-298A-526	Sequence 526, App
28	3824.5	89.3	736	10	US-09-978-188A-526	Sequence 526, App
29	3824.5	89.3	736	10	US-09-978-681A-526	Sequence 526, App
30	3824.5	89.3	736	10	US-09-978-194A-526	Sequence 526, App
31	3824.5	89.3	736	10	US-09-999-829A-526	Sequence 526, App
32	3824.5	89.3	736	10	US-09-978-299A-526	Sequence 526, App
33	3824.5	89.3	736	10	US-09-978-544A-526	Sequence 526, App
34	3824.5	89.3	736	10	US-09-978-665A-526	Sequence 526, App
35	3824.5	89.3	736	10	US-09-978-802A-526	Sequence 526, App
36	3824.5	89.3	736	12	US-10-164-749A-526	Sequence 526, App
37	3824.5	89.3	736	12	US-10-206-915-420	Sequence 420, App
38	3824.5	89.3	736	12	US-10-199-670-420	Sequence 420, App
39	3824.5	89.3	736	12	US-10-201-858-420	Sequence 420, App
40	3824.5	89.3	736	12	US-09-999-831A-526	Sequence 526, App
41	3824.5	89.3	736	12	US-10-205-890-420	Sequence 420, App
42	3824.5	89.3	736	12	US-10-208-024-420	Sequence 420, App
43	3824.5	89.3	736	12	US-10-201-853-420	Sequence 420, App
44	3824.5	89.3	736	12	US-10-013-917A-526	Sequence 526, App
45	3824.5	89.3	736	12	US-10-174-581-420	Sequence 420, App

## ALIGNMENTS

RESULT 1  
US-10-267-502-253  
; Sequence 253, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267, 502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 253  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-267-502-253

Query Match 100.0%; Score 4281; DB 12; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNVALGELGAGSNMVEYKRA	12	US-10-267-502-253	Sequence 253, App
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DB	61	GTPRSGLTWRVTCPIRLRSISGICSTWVGFGQKTRQLLSGRQLFLVLAGASLLLAALL	120		
QY	121	LGCLVVALGYQVRDPSHSTCTFACCRVAGKILIESLDKGVSPCEPDYQSPSCGWMIRNP	180		
DB	121	LGCLVVALGYQVRDPSHSTCTFACCRVAGKILIESLDKGVSPCEPDYQSPSCGWMIRNP	180		
QY	181	PDGRSMNTFNSIMDNOALILKRLLENTFNSSEABOKTORFYISCLQVERIEBELGAOP	240		
DB	181	PDGRSMNTFNSIMDNOALILKRLLENTFNSSEABOKTORFYISCLQVERIEBELGAOP	240		

QY 241 LRDLEKIGGMNITGPMDDNFMENVLKAVAGTYRATPFYVYISADSKSSNVIOVDS 300  
DB 241 LRDLEKIGGMNITGPMDDNFMENVLKAVAGTYRATPFYVYISADSKSSNVIOVDS 300  
QY 301 GFLPSRDYLLNRTANEKVLTAVALDYMEELGMLGGPSTREOMQVLELEIOLANTIV 360  
DB 301 GFLPSRDYLLNRTANEKVLTAVALDYMEELGMLGGPSTREOMQVLELEIOLANTIV 360  
QY 361 PODQRDEEKIYHKMSISELOALAPSDMWLEFLSFLSPLSDSEPVVYVGYMDYLOQVS 420  
DB 361 PODQRDEEKIYHKMSISELOALAPSDMWLEFLSFLSPLSDSEPVVYVGYMDYLOQVS 420  
QY 421 ELINRTEPSILNNYLLMNLVOKTSSLDREFSAOEKLETLVGTCKSCVPRMOTCISNT 480  
DB 421 ELINRTEPSILNNYLLMNLVOKTSSLDREFSAOEKLETLVGTCKSCVPRMOTCISNT 480  
QY 481 DDALGALGSLFYKATFDROSKIEAGMISEIRTAFEALGOLVMMDEKTRQAAEKADA 540  
DB 481 DDALGALGSLFYKATFDROSKIEAGMISEIRTAFEALGOLVMMDEKTRQAAEKADA 540  
QY 541 IYDMIGPPDFILPEKELDDYDVEISEDSFQNMNLNYSFAKWADQLRKPSRDWS 600  
DB 541 IYDMIGPPDFILPEKELDDYDVEISEDSFQNMNLNYSFAKWADQLRKPSRDWS 600  
QY 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARNHPKALNPGGIGVMGHELTAFDQGRE 660  
DB 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARNHPKALNPGGIGVMGHELTAFDQGRE 660  
QY 661 YDKEGMLRPMWQNESLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 720  
DB 661 YDKEGMLRPMWQNESLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 720  
QY 721 NAYKAWLRKHGEEOQLPAVGLTNHOLFVGFPAQVCSVTPRESSHEGLVTDHSPARFRV 780  
DB 721 NAYKAWLRKHGEEOQLPAVGLTNHOLFVGFPAQVCSVTPRESSHEGLVTDHSPARFRV 780  
QY 781 LGTLSNRDPLRHFPGCVGSPMNPQGLCEW 811  
DB 781 LGTLSNRDPLRHFPGCVGSPMNPQGLCEW 811

RESULT 2  
US-10-273-992-2  
; Sequence 2, Application US/10273992  
; Publication No. US20030129700A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al.  
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES  
; TITLE OF INVENTION: THERMOP  
; FILE REFERENCE: C1001200DIV  
; CURRENT APPLICATION NUMBER: US/10/273.992  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 811  
; TYPE: PRT  
; ORGANISM: Human  
US-10-273-992-2

Query Match 100.0%; Score 4281; DB 14; Length 811;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MVALOELGAGSNMVEYKATLRDEDAPEFVPEGASPDAMEYKAGSPSPSPGMP 60  
QY 61 GTPRSSGLFWRVTCPHIRISISGLCSRTMVGFOKTRQLLSRTQLBELVLGASILLAA 120  
DB 61 GTPRSSGLFWRVTCPHIRISISGLCSRTMVGFOKTRQLLSRTQLBELVLGASILLAA 120

QY 121 LGCLVALGQYHRDPSHSTCLTEACIRVAGKILIESLDKGVSPCEDFYQSCGGMIRBNPL 180  
DB 121 LGCLVALGQYHRDPSHSTCLTEACIRVAGKILIESLDKGVSPCEDFYQSCGGMIRBNPL 180  
QY 181 PGRSRMNTFNSLMDQNALHLLLENTFNSSSEAOQTORFYLSCLOVERIBEIGAOP 240  
DB 181 PGRSRMNTFNSLMDQNALHLLLENTFNSSSEAOQTORFYLSCLOVERIBEIGAOP 240  
QY 241 LRDLEKIGGMNITGPMDDNFMENVLKAVAGTYRATPFYVYISADSKSSNVIOVDS 300  
DB 241 LRDLEKIGGMNITGPMDDNFMENVLKAVAGTYRATPFYVYISADSKSSNVIOVDS 300  
QY 301 GFLPSRDYLLNRTANEKVLTAVALDYMEELGMLGGPSTREOMQVLELEIOLANTIV 360  
DB 301 GFLPSRDYLLNRTANEKVLTAVALDYMEELGMLGGPSTREOMQVLELEIOLANTIV 360  
QY 361 PODQRDEEKIYHKMSISELOALAPSDMWLEFLSFLSPLSDSEPVVYVGYMDYLOQVS 420  
DB 361 PODQRDEEKIYHKMSISELOALAPSDMWLEFLSFLSPLSDSEPVVYVGYMDYLOQVS 420  
QY 421 ELINRTEPSILNNYLLMNLVOKTSSLDREFSAOEKLETLVGTCKSCVPRMOTCISNT 480  
DB 421 ELINRTEPSILNNYLLMNLVOKTSSLDREFSAOEKLETLVGTCKSCVPRMOTCISNT 480  
QY 481 DDALGALGSLFYKATFDROSKIEAGMISEIRTAFEALGOLVMMDEKTRQAAEKADA 540  
DB 481 DDALGALGSLFYKATFDROSKIEAGMISEIRTAFEALGOLVMMDEKTRQAAEKADA 540  
QY 541 IYDMIGPPDFILPEKELDDYDVEISEDSFQNMNLNYSFAKWADQLRKPSRDWS 600  
DB 541 IYDMIGPPDFILPEKELDDYDVEISEDSFQNMNLNYSFAKWADQLRKPSRDWS 600  
QY 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARNHPKALNPGGIGVMGHELTAFDQGRE 660  
DB 601 MPTQYNAAYLLPTKNEIVFPAGILOAPFYARNHPKALNPGGIGVMGHELTAFDQGRE 660  
QY 661 YDKEGMLRPMWQNESLAAPRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 720  
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QY 721 NAYKAWLRKHGEEOQLPAVGLTNHOLFVGFPAQVCSVTPRESSHEGLVTDHSPARFRV 780  
DB 721 NAYKAWLRKHGEEOQLPAVGLTNHOLFVGFPAQVCSVTPRESSHEGLVTDHSPARFRV 780  
QY 781 LGTLSNRDPLRHFPGCVGSPMNPQGLCEW 811  
DB 781 LGTLSNRDPLRHFPGCVGSPMNPQGLCEW 811

RESULT 3  
US-09-888-615-80  
; Sequence 80, Application US/09888615  
; Patent No. US2002064856A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOMAN, GREGORY  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: CAENEPEEL, SEAN  
; APPLICANT: CHARYDCAZAK, GLEN  
; APPLICANT: MANNING, GERRARD  
; APPLICANT: SUDARSANAM, SUCHA  
; TITLE OF INVENTION: NOVEL PROTEASES  
; FILE REFERENCE: 038602/1214  
; CURRENT APPLICATION NUMBER: US/09/888.615  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: 60/214,047  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 80  
; LENGTH: 765  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-888-615-80

Query Match 93.3%; Score 3993; DB 9; Length 765;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

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DB 1 MNVALDELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEVGKASPPSPGMP 60
QY 61 GTPRSSGLFWRVYCPHRLRSISGLCSRTMWGFOKTRQLLSRTQLELVLAGASILLALL 120
DB 43 -----VFQKGTQLLSRTQLELVLAGASILLALL 74
QY 121 LGCLVALGYQYHRDPSHSTCLTEACTIRVAGKILIESIDRGVSPCEDFYQSCGGMIRRNPL 180
DB 75 LGCLVALGYQYHRDPSHSTCLTEACTIRVAGKILIESIDRGVSPCEDFYQSCGGMIRRNPL 134
QY 181 PDGRSMNTFNSLMDQNOAILKHLLENTFNSSSEAOQTQRPYLSCLQVERIEELGAOP 240
DB 135 PDGRSMNTFNSLMDQNOAILKHLLENTFNSSSEAOQTQRPYLSCLQVERIEELGAOP 194
QY 241 LRDLEIKIGMNTTGMWDQNFMEVYKAVAGTYRATPFTVYISADSKSNSNVIQVDS 300
DB 195 LRDLEIKIGMNTTGMWDQNFMEVYKAVAGTYRATPFTVYISADSKSNSNVIQVDS 254
QY 301 GLFLPSRDYILNRTANEKYLTAIYDYMEELGMLGSRPTSTREMOQOVLLEIOLANITY 360
DB 255 GLFLPSRDYILNRTANEKYLTAIYDYMEELGMLGSRPTSTREMOQOVLLEIOLANITY 314
QY 361 PDORDEEKIYHKMSISELOALAPSMDLLEFLSLSPLELSDSEPPVVVYGNDYIQVS 420
DB 315 PDORDEEKIYHKMSISELOALAPSMDLLEFLSLSPLELSDSEPPVVVYGNDYIQVS 374
QY 421 ELINRTEPSILNNYILNVLVQKTTSLDRFPESAQKLETLVYGTKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNYILNVLVQKTTSLDRFPESAQKLETLVYGTKSCVPRMOTCISNT 434
QY 481 DDALGFALGSLFVKATFDRQSKELAEGLMISEIRTAEEALGOLVWMDKTRQAAKEKADA 540
DB 435 DDALGFALGSLFVKATFDRQSKELAEGLMISEIRTAEEALGOLVWMDKTRQAAKEKADA 494
QY 541 IYDMIGFPDPILEPKELDVYDYEISEDSFQNMMLNLYNFSKAWAADLRRPSPSDQNS 600
DB 495 IYDMIGFPDPILEPKELDVYDYEISEDSFQNMMLNLYNFSKAWAADLRRPSPSDQNS 554
QY 601 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHELTTHAFDDQGRE 660
DB 555 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHELTTHAFDDQGRE 614
QY 661 YXKEGMLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 720
DB 615 YXKEGMLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 674
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWCVSVPTESSHEGLVTDPHSPARFRV 780
DB 675 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWCVSVPTESSHEGLVTDPHSPARFRV 734
QY 781 LGTILNSRDPLRHFGCPVGSPPMNPQOLCEVW 811
DB 735 LGTILNSRDPLRHFGCPVGSPPMNPQOLCEVW 765
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RESULT 4  
US-10-273-992-4

; Sequence 4, Application US/10273992

; Publication No. US20030129700A1

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al.

; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

; FILE REFERENCE: CL001200DIV

CURRENT APPLICATION NUMBER: US/10/273,992

CURRENT FILING DATE: 2002-10-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 765

TYPE: PRT

ORGANISM: Human

US-10-273-992-4

Query Match 93.3%; Score 3993; DB 14; Length 765;

Best Local Similarity 94.3%; Pred. No. 0;

Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

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QY 1 MNVALDELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEVGKASPPSPGMP 60
DB 1 MNVALDELGAGSNMVEYKRAITLRDEDAPEPTVEGASPDAMEVGKASPPSPGMP 42
QY 61 GTPRSSGLFWRVYCPHRLRSISGLCSRTMWGFOKTRQLLSRTQLELVLAGASILLALL 120
DB 43 -----VFQKGTQLLSRTQLELVLAGASILLALL 74
QY 121 LGCLVALGYQYHRDPSHSTCLTEACTIRVAGKILIESIDRGVSPCEDFYQSCGGMIRRNPL 180
DB 75 LGCLVALGYQYHRDPSHSTCLTEACTIRVAGKILIESIDRGVSPCEDFYQSCGGMIRRNPL 134
QY 181 PDGRSMNTFNSLMDQNOAILKHLLENTFNSSSEAOQTQRPYLSCLQVERIEELGAOP 240
DB 135 PDGRSMNTFNSLMDQNOAILKHLLENTFNSSSEAOQTQRPYLSCLQVERIEELGAOP 194
QY 241 LRDLEIKIGMNTTGMWDQNFMEVYKAVAGTYRATPFTVYISADSKSNSNVIQVDS 300
DB 195 LRDLEIKIGMNTTGMWDQNFMEVYKAVAGTYRATPFTVYISADSKSNSNVIQVDS 254
QY 301 GLFLPSRDYILNRTANEKYLTAIYDYMEELGMLGSRPTSTREMOQOVLLEIOLANITY 360
DB 255 GLFLPSRDYILNRTANEKYLTAIYDYMEELGMLGSRPTSTREMOQOVLLEIOLANITY 314
QY 361 PDORDEEKIYHKMSISELOALAPSMDLLEFLSLSPLELSDSEPPVVVYGNDYIQVS 420
DB 315 PDORDEEKIYHKMSISELOALAPSMDLLEFLSLSPLELSDSEPPVVVYGNDYIQVS 374
QY 421 ELINRTEPSILNNYILNVLVQKTTSLDRFPESAQKLETLVYGTKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNYILNVLVQKTTSLDRFPESAQKLETLVYGTKSCVPRMOTCISNT 434
QY 481 DDALGFALGSLFVKATFDRQSKELAEGLMISEIRTAEEALGOLVWMDKTRQAAKEKADA 540
DB 435 DDALGFALGSLFVKATFDRQSKELAEGLMISEIRTAEEALGOLVWMDKTRQAAKEKADA 494
QY 541 IYDMIGFPDPILEPKELDVYDYEISEDSFQNMMLNLYNFSKAWAADLRRPSPSDQNS 600
DB 495 IYDMIGFPDPILEPKELDVYDYEISEDSFQNMMLNLYNFSKAWAADLRRPSPSDQNS 554
QY 601 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHELTTHAFDDQGRE 660
DB 555 MTPQTVNAYYLLPTKNEIVPPAGILOAPFYARNHPKALNFGGIGVNGHELTTHAFDDQGRE 614
QY 661 YXKEGMLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 720
DB 615 YXKEGMLRPMWQNESIAAFRNHTACMEBOYNOYVNGERLNGRQTLGENIADNGGLKAA 674
QY 721 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWCVSVPTESSHEGLVTDPHSPARFRV 780
DB 675 NAYKAMLRKHGEEQOLPAVGLTNHOLFVYGAQVWCVSVPTESSHEGLVTDPHSPARFRV 734
QY 781 LGTILNSRDPLRHFGCPVGSPPMNPQOLCEVW 811
DB 735 LGTILNSRDPLRHFGCPVGSPPMNPQOLCEVW 765
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RESULT 5

US-10-453-764-2

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Sequence 2, Application US/10453764
Publication No. US20030232044A1
GENERAL INFORMATION:
APPLICANT: White, David
TITLE OF INVENTION: USE FOR ENDOTHELIN CONVERTING ENZYME 2
TITLE OF INVENTION: (ECC-2) IN THE DIAGNOSIS AND TREATMENT OF METABOLIC
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: MP102-2661RM
CURRENT APPLICATION NUMBER: US/10/453,764
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 60/386,333
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 765
TYPE: PRN
ORGANISM: Homo sapiens
US-10-453-764-2

Query Match      93.3%; Score 3993; DB 15; Length 765;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

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DB 1 MNAVALDELGASNNVEYKATLRDEDAPEPTVEGASPDAMEYKGSPPSPGMP 42
QY 61 GTPRSSGGLFWRVTCPLRLSISGLCSRTWVGFOKTRQLGSRQLQLEIVLAGSLIAALL 120
DB 43 -----VFQKTRQLGSRQLQLEIVLAGSLIAALL 74
QY 121 LGGLVALGVQYHRDPSSHSTCLTEACTRVACKTIIESLDRGVSPCEDFQSCGMMIRNPL 180
DB 75 LGGLVALGVQYHRDPSSHSTCLTEACTRVACKTIIESLDRGVSPCEDFQSCGMMIRNPL 134
QY 181 PDGRSSMNTFNSLMDONQALIKHLLENTFNSSSEAEQKQRYLSCLQYERIEEAGAP 240
DB 135 PDGRSSMNTFNSLMDONQALIKHLLENTFNSSSEAEQKQRYLSCLQYERIEEAGAP 194
QY 241 LRDLIEKIGMNTTGPWDQDNFMEVLKAVAGYRATPEFTVYISADSKSSNVIOVDOS 300
DB 195 LRDLIEKIGMNTTGPWDQDNFMEVLKAVAGYRATPEFTVYISADSKSSNVIOVDOS 254
QY 301 GLELPRDYLYANTANEKUTAYLDVMEELGMLGGPSTSTRMOQVLELEIOLANTIV 360
DB 255 GLELPRDYLYANTANEKUTAYLDVMEELGMLGGPSTSTRMOQVLELEIOLANTIV 314
QY 361 PDQRDEDEKTYHKMSISELOALAPSMWLEFLSFLSPLELSDSEPVVYVYGMVYLOQVS 420
DB 315 PDQRDEDEKTYHKMSISELOALAPSMWLEFLSFLSPLELSDSEPVVYVYGMVYLOQVS 374
QY 421 ELINRTEPSILNNVLIWNLVQKTTSSIDRRPESAOEKLFTLYGTXKSCVPRMOTCISNT 480
DB 375 ELINRTEPSILNNVLIWNLVQKTTSSIDRRPESAOEKLFTLYGTXKSCVPRMOTCISNT 434
QY 481 DDALGFLGSLFKATPDROSKEIABEMISEIRTAPEALGOLVWMDKTRQAKKEXADA 540
DB 435 DDALGFLGSLFKATPDROSKEIABEMISEIRTAPEALGOLVWMDKTRQAKKEXADA 494
QY 541 IYDMIGPDPILPEKELDDVDGEIASEDSFFQNMNLVNFSAKVMAADQARKPSRDQMS 600
DB 495 IYDMIGPDPILPEKELDDVDGEIASEDSFFQNMNLVNFSAKVMAADQARKPSRDQMS 554
QY 601 MTPQTVNAYYLLPTKNEIIVPAGILQAFYARNHPKALNFGSIGVWGHETLTHAFDDQRE 660
DB 555 MTPQTVNAYYLLPTKNEIIVPAGILQAFYARNHPKALNFGSIGVWGHETLTHAFDDQRE 614
QY 661 YDEEGNLRPWWQNESLAAFRNHTACMEQYNOYVNGERLINGQTLGENTADNGGLKAAAY 720
DB 615 YDEEGNLRPWWQNESLAAFRNHTACMEQYNOYVNGERLINGQTLGENTADNGGLKAAAY 674
QY 721 NAYKAWMLRKGEEOQLPAVGLTNHQLFFVGFPAQVWCSTVPRESSHGLVTDPHSPARFRV 780
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DB 675 NAYKAWMLRKGEEOQLPAVGLTNHQLFFVGFPAQVWCSTVPRESSHGLVTDPHSPARFRV 734
QY 781 LGTILNSRDLRHFHGFPGVSSPMNPQOLCEW 811
DB 735 LGTILNSRDLRHFHGFPGVSSPMNPQOLCEW 765

RESULT 6
US-09-978-295A-526
Sequence 526, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Kljavin, Ivar J.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 9; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VFQKGTROLLGSRQLELVYLAGASLLAAALLGTVLVAGVYHRDPESHSTCTEACTIRV 148  
DB 14 VFQKGTROLLGSRQLELVYLAGASLLAAALLGTVLVAGVYHRDPESHSTCTEACTIRV 73



QY 149 AGKILSLDRGVSPCEDFYQSCGWMIRBNPLPDGSRMNTFNSLMDQOALIKHLLENT 208  
DB 74 AKLIESLDRGVSPCEDFYQSCGWMIRBNPLPDGSRMNTFNSLMDQOALIKHLLENT 133  
QY 209 TNNSSSEABOKTORFYLSCLQVERIBELGAOPLRDLIEKIGMNTGPPDQONFMEVTKA 268  
DB 134 TNNSSSEABOKTORFYLSCLQVERIBELGAOPLRDLIEKIGMNTGPPDQONFMEVTKA 193  
QY 269 VAGTRATPFYTVYISADSKSSNSVYQVDSGLPLPSRDYILNRTANKVLTAYLDYME 328  
DB 194 VAGTRATPFYTVYISADSKSSNSVYQVDSGLPLPSRDYILNRTANKVLTAYLDYME 253  
QY 339 ELGMLLGRPTSTREOMQOVLLELLOLANITVPODRDEBKLYHMSISELOALAPSD 388  
DB 254 ELGMLLGRPTSTREOMQOVLLELLOLANITVPODRDEBKLYHMSISELOALAPSD 313  
QY 389 WLEPLSLPLSLSDSPVVVYGYMDYLOQVSELNRTPESTLNNYLTNNLYQKTTSSLD 448  
DB 314 WLEPLSLPLSLSDSPVVVYGYMDYLOQVSELNRTPESTLNNYLTNNLYQKTTSSLD 373  
QY 449 RRPESAOELFTVYGTKKSCVPRMOTCSMTDDALGFALGSLFYKATFDRSKETABGM 508  
DB 374 RRPESAOELFTVYGTKKSCVPRMOTCSMTDDALGFALGSLFYKATFDRSKETABGM 433  
QY 509 ISEIRTAPEALGOLVMDKTRQAAKERADAIYDMIGPPDLLEPKELDYYDYEISE 568  
DB 434 ISEIRTAPEALGOLVMDKTRQAAKERADAIYDMIGPPDLLEPKELDYYDYEISE 493  
QY 569 DSFPOMLNLVNSAKVMADQLRKPPSRDQMSMTPTVNAVYLPKNEIVPAGIIOAPF 628  
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QY 629 YARNHPKANFGGIGVVMHHELTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 688  
DB 554 YARNHPKANFGGIGVVMHHELTHAFDDGREYDEKGNLRPMWONESLAFRNHTACME 613  
QY 689 QYNQOVNERLNGRQTLGENTADNGGLKAAVYAKMLRKGEEOQLPAVGLTNHQLFF 748  
DB 614 QYNQOVNERLNGRQTLGENTADNGGLKAAVYAKMLRKGEEOQLPAVGLTNHQLFF 673  
QY 749 VGFPAQWCVTRTPESHGELVTDPHSPARFVIGTISNRDPLRHFGEVGSFPMNGQLC 808  
DB 674 VGFPAQWCVTRTPESHGELVTDPHSPARFVIGTISNRDPLRHFGEVGSFPMNGQLC 733  
QY 809 EYM 811  
DB 734 EYM 736

RESULT 7  
US-09-978-697-526

Sequence 526, Application US/09978697  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferreira, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Auestin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P/C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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Query Match 89.3%; Score 3824.5; DB 9; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
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149 AGKILESIDRGVSPCEDFYQSCGGMIRNPLPDGRSRMTFNSLMDQOAILKHLNLT 208  
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209 TNSSSSEAEQKQRYLLSCQYERIEELGAOPLRDLIEKIGMNITGPPDQDNFMEVTKA 268  
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389 WLEPLSPILSPLELSDSEPVVYVYGMVYIQVSELINRTEPSILNNYLIWNLVQKTTSSLD 448  
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Db	554	YARNHPKALNFGIGIGVMMHELTTHAFDDGREYDKGNLRPMQNSLAAFRNHTCMEE	613
Qy	669	QYNQOVNGERLNGRQTLTGENTADNGGLKAAVNAVYAMLRKHGEBOQLPAVGLTNHQLFF	748
Db	614	QYNQOVNGERLNGRQTLTGENTADNGGLKAAVNAVYAMLRKHGEBOQLPAVGLTNHQLFF	673
Qy	749	VGFPAQWCVCVRTPESHSBGLVYDPHSPARFVLTGSNSHDFLRHRCGPVGSFMRNQCQLC	808
Db	674	VGFPAQWCVCVRTPESHSBGLVYDPHSPARFVLTGSNSHDFLRHRCGPVGSFMRNQCQLC	733
Qy	809	EVW 811	
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GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi			
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
TITLE OF INVENTION: Acids Encoding the Same			
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 9; Length 736;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 14 VGFQKGTROLLGSRTOLEVLVAGASILLALLGLGCLVALGVQYHRDPHSSTCLTEACIRV 73  
 QY 149 AGKILESIDRGVSPCCDFYQSCGWIIRRNPLPDGSRNNTFMSLDQNALIKHLENT 208  
 DB 74 AGKILESIDRGVSPCCDFYQSCGWIIRRNPLPDGSRNNTFMSLDQNALIKHLENT 133  
 QY 209 TFFSSSEAEOKTORFYLSCLOVERISELAQPLRDLIEKIGGNITGPMODFMELKA 268  
 DB 134 TFFSSSEAEOKTORFYLSCLOVERISELAQPLRDLIEKIGGNITGPMODFMELKA 193  
 QY 269 VAGTYRATPFFTYIISADSKSSNSNVIQVDQSLFLPSRDYILNRITANEKVLTAVIDYME 328  
 DB 194 VAGTYRATPFFTYIISADSKSSNSNVIQVDQSLFLPSRDYILNRITANEKVLTAVIDYME 253  
 QY 329 ELGMLIGRPTSTREQMOQVLBLEIOLANITVPQDRDBEKIYHKMSISELOALAPSM 388  
 DB 254 ELGMLIGRPTSTREQMOQVLBLEIOLANITVPQDRDBEKIYHKMSISELOALAPSM 313  
 QY 389 WLEFLSFLSPLSDSEPVVYGMQYLOQVSELINRTEPSILNNYLIWNLVOKTSSLD 448  
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 QY 749 VGEPAQWCSVTPRESHEGLVTDPSPARFVLGTLSNSRDLRHHGCVGSPMNGOJC 808  
 DB 674 VGEPAQWCSVTPRESHEGLVTDPSPARFVLGTLSNSRDLRHHGCVGSPMNGOJC 733  
 QY 809 EYM 811  
 DB 734 EYM 736

RESULT 9  
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 Sequence 526, Application US/09999832A  
 Publication No. US20020192706A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, Jamesi  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
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 DB 14 VGFQKGTROLGSRTOLEVLGASILLALLLGCVLALGVQYHRDPSHSTCLTEACIRV 73  
 QY 149 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGSRNMTFNSLMDQNALIKHILENT 208  
 DB 74 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGSRNMTFNSLMDQNALIKHILENT 133  
 QY 209 TENSSEAEOKTORFYLSCLQVERIEBELGAOPLRDLIEKIGWNITGPMQDNFMVYLKA 268  
 DB 134 TENSSEAEOKTORFYLSCLQVERIEBELGAOPLRDLIEKIGWNITGPMQDNFMVYLKA 193  
 QY 269 VAGTYATPFTFYISADSKSSNSNYIOVQSGFLPSRDYLNRTANEKVLTAVIDYME 328  
 DB 194 VAGTYATPFTFYISADSKSSNSNYIOVQSGFLPSRDYLNRTANEKVLTAVIDYME 253  
 QY 329 ELGMLLGRPTSTREMOQVLELEIOLANITVPQDGRDEEKIYHKMSISELOALAPSM 388  
 DB 254 ELGMLLGRPTSTREMOQVLELEIOLANITVPQDGRDEEKIYHKMSISELOALAPSM 313  
 QY 389 WLEFLSFLSPLELSDSEPVVYVGM DYLOQVSELINRTEPSILNNYILNVLVOKTSSLD 448  
 DB 314 WLEFLSFLSPLELSDSEPVVYVGM DYLOQVSELINRTEPSILNNYILNVLVOKTSSLD 373  
 QY 449 RRESAOKELLETLYGKKSCVPRMOTCISNTDDALGFALGSLFYKATPRROSKETAEGM 508  
 DB 374 RRESAOKELLETLYGKKSCVPRMOTCISNTDDALGFALGSLFYKATPRROSKETAEGM 433  
 QY 509 ISEIRTAFFEBALGOLVWMDKTRQAAKAKADAIYDMIGFDPFLPEKELDDVDGYEISE 568  
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 QY 569 DSFFQNMNLNYSASAKVADOLKRPGRDQSMTPOTVNAVYLPPTKNEIYFPAIGIQAFF 628  
 DB 494 DSFFQNMNLNYSASAKVADOLKRPGRDQSMTPOTVNAVYLPPTKNEIYFPAIGIQAFF 553  
 QY 629 YANNHKALNFGIGIYVNGHELTHAPDDQREYDKGNLAPWQNSLAFRNHTACME 688  
 DB 554 YANNHKALNFGIGIYVNGHELTHAPDDQREYDKGNLAPWQNSLAFRNHTACME 613  
 QY 689 QYQYQVNGERLNGRQTLGENDIADNGCLKAAYNAAYKWLKRGEBQOLPAVGLTNHOLF 748  
 DB 614 QYQYQVNGERLNGRQTLGENDIADNGCLKAAYNAAYKWLKRGEBQOLPAVGLTNHOLF 673  
 QY 749 VGEAQWCVSRTPRESSHEGLVTDPHSPARFVLTLSNSRDLRHFQCPVGSPPNQCQLC 808  
 DB 674 VGEAQWCVSRTPRESSHEGLVTDPHSPARFVLTLSNSRDLRHFQCPVGSPPNQCQLC 723  
 QY 809 EYW 811  
 DB 734 EYW 736

RESULT 11  
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 ; Sequence 526, Application US/09978608A  
 ; Publication No. US20030045462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austen L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavitt, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630PIC22  
 ; CURRENT APPLICATION NUMBER: US/09/978,608A  
 ; CURRENT FILING DATE: 2001-10-16  
 ; NUMBER OF SEQ ID NOS: 624  
 ; Prior Application removed - See File Wrapper or Palm  
 ; SEQ ID NO 526  
 ; LENGTH: 736  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-978-608A-526

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
 Best Local Similarity: 99.9%; Pred. No. 0;  
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGTROLGSRTOLEVLGASILLALLLGCVLALGVQYHRDPSHSTCLTEACIRV 148  
 DB 14 VGFQKGTROLGSRTOLEVLGASILLALLLGCVLALGVQYHRDPSHSTCLTEACIRV 73  
 QY 149 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGSRNMTFNSLMDQNALIKHILENT 208  
 DB 74 AGKILSLDRGVSPCEDFYQFSCGWIIRNPLPDGSRNMTFNSLMDQNALIKHILENT 133  
 QY 209 TENSSEAEOKTORFYLSCLQVERIEBELGAOPLRDLIEKIGWNITGPMQDNFMVYLKA 268  
 DB 134 TENSSEAEOKTORFYLSCLQVERIEBELGAOPLRDLIEKIGWNITGPMQDNFMVYLKA 193  
 QY 269 VAGTYATPFTFYISADSKSSNSNYIOVQSGFLPSRDYLNRTANEKVLTAVIDYME 328  
 DB 194 VAGTYATPFTFYISADSKSSNSNYIOVQSGFLPSRDYLNRTANEKVLTAVIDYME 253  
 QY 329 ELGMLLGRPTSTREMOQVLELEIOLANITVPQDGRDEEKIYHKMSISELOALAPSM 388  
 DB 254 ELGMLLGRPTSTREMOQVLELEIOLANITVPQDGRDEEKIYHKMSISELOALAPSM 313  
 QY 389 WLEFLSFLSPLELSDSEPVVYVGM DYLOQVSELINRTEPSILNNYILNVLVOKTSSLD 448  
 DB 314 WLEFLSFLSPLELSDSEPVVYVGM DYLOQVSELINRTEPSILNNYILNVLVOKTSSLD 373  
 QY 449 RRESAOKELLETLYGKKSCVPRMOTCISNTDDALGFALGSLFYKATPRROSKETAEGM 508  
 DB 374 RRESAOKELLETLYGKKSCVPRMOTCISNTDDALGFALGSLFYKATPRROSKETAEGM 433  
 QY 509 ISEIRTAFFEBALGOLVWMDKTRQAAKAKADAIYDMIGFDPFLPEKELDDVDGYEISE 568

Db 434 ISEIRTAFFEBALGOLVWMDKTRQAAKEKADAIYDMIGPDPFLBPEKELDDVYDGEISE 493  
QY 569 DSEFQNMNLNYSASVAMADOLRKPPSRDQMSMTPTQVNAVYLPTNKEIVFPAGILQAPF 628  
Db 494 DSEFQNMNLNYSASVAMADOLRKPPSRDQMSMTPTQVNAVYLPTNKEIVFPAGILQAPF 553  
QY 629 YARNHFKALNFGGIGVVMGHELTTHAFDDQREYDKEGNLRPMWQNESLAAFRNHTACMEB 688  
Db 554 YARNHFKALNFGGIGVVMGHELTTHAFDDQREYDKEGNLRPMWQNESLAAFRNHTACMEB 613  
QY 689 QYNQYOVNGBRLNGRQTLGENTADNGGLKAAVNAVYAMLRKGEBOQLPAVGLTNHQLF 748  
Db 614 QYNQYOVNGBRLNGRQTLGENTADNGGLKAAVNAVYAMLRKGEBOQLPAVGLTNHQLF 673  
QY 749 VGEAOWMCSVRTPESSHEGLVTDPHSPARFRVILGTLNSRDFLRHGCPCVGSPPMNGQLC 808  
Db 674 VGEAOWMCSVRTPESSHEGLVTDPHSPARFRVILGTLNSRDFLRHGCPCVGSPPMNGQLC 733  
QY 809 EVW 811  
Db 734 EVW 736

RESULT 12  
US-09-978-585A-526  
; Sequence 526, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavijn, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James J.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumaer, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC5  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 526  
; LENGTH: 736  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-585A-526

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGEOKGTRQLGSRQLELVLAGASLLAALLGCLVALGVYHRDPSHSTCLTEACTIV 148

Db 14 VGEOKGTRQLGSRQLELVLAGASLLAALLGCLVALGVYHRDPSHSTCLTEACTIV 73  
QY 149 AGKILLESILRGVSPCEDFVQSCGGWIRBNPLPDGRSRNNTNSLMDQOAILKHLLENT 208  
Db 74 AGKILLESILRGVSPCEDFVQSCGGWIRBNPLPDGRSRNNTNSLMDQOAILKHLLENT 133  
QY 209 TNSNSEAEQKQRFYLSCLQYERIEELGAQPLRLDLEIKGMINITGPMQDNFMEVLKA 268  
Db 134 TNSNSEAEQKQRFYLSCLQYERIEELGAQPLRLDLEIKGMINITGPMQDNFMEVLKA 193  
QY 269 VAGTRATPFTFYVISADSKSSNSVITQVDSGLFSPSDYILNRTANEKVLTAIYDIYE 328  
Db 194 VAGTRATPFTFYVISADSKSSNSVITQVDSGLFSPSDYILNRTANEKVLTAIYDIYE 253  
QY 329 ELGMLIGRPTSTRMOQVLELEIOLANITVPODRRDEEKIYHMSISELOALAPSD 388  
Db 254 ELGMLIGRPTSTRMOQVLELEIOLANITVPODRRDEEKIYHMSISELOALAPSD 313  
QY 389 WLEFLSFLSPLSELSDSEPVVYGMVDYLOVSELINRTEPSILNNYLIWNLVQKTTSSLD 448  
Db 314 WLEFLSFLSPLSELSDSEPVVYGMVDYLOVSELINRTEPSILNNYLIWNLVQKTTSSLD 373  
QY 449 RRPESAQEKLETLVYTKKSCVPRWQTCISNTDDALGFALGSLFYKATFDROSKETAEQM 508  
Db 374 RRPESAQEKLETLVYTKKSCVPRWQTCISNTDDALGFALGSLFYKATFDROSKETAEQM 433  
QY 509 ISEIRTAFFEBALGOLVWMDKTRQAAKEKADAIYDMIGPDPFLBPEKELDDVYDGEISE 568  
Db 434 ISEIRTAFFEBALGOLVWMDKTRQAAKEKADAIYDMIGPDPFLBPEKELDDVYDGEISE 493  
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Db 494 DSEFQNMNLNYSASVAMADOLRKPPSRDQMSMTPTQVNAVYLPTNKEIVFPAGILQAPF 553  
QY 629 YARNHFKALNFGGIGVVMGHELTTHAFDDQREYDKEGNLRPMWQNESLAAFRNHTACMEB 688  
Db 554 YARNHFKALNFGGIGVVMGHELTTHAFDDQREYDKEGNLRPMWQNESLAAFRNHTACMEB 613  
QY 689 QYNQYOVNGBRLNGRQTLGENTADNGGLKAAVNAVYAMLRKGEBOQLPAVGLTNHQLF 748  
Db 614 QYNQYOVNGBRLNGRQTLGENTADNGGLKAAVNAVYAMLRKGEBOQLPAVGLTNHQLF 673  
QY 749 VGEAOWMCSVRTPESSHEGLVTDPHSPARFRVILGTLNSRDFLRHGCPCVGSPPMNGQLC 808  
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QY 809 EVW 811  
Db 734 EVW 736

RESULT 13  
US-09-978-191A-526  
; Sequence 526, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: US/09/978,191A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 10; Length 736;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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14 VGFQKTRQLLGSRTQLELVLAGASLLALLLGGVVALGVYHRDPSHSTCTEACIRV 73  
149 AGKILSLDRGVSPCEPFYQFSCGWRTRNPLPDGRSRMTTPNSIMQONAILKHILENT 208  
74 AGKILSLDRGVSPCEPFYQFSCGWRTRNPLPDGRSRMTTPNSIMQONAILKHILENT 133  
209 TPNSSSAEQKOTQRFYSCLOVERIEELGAOPLRDLLEKIGNNITGPMQDNFMEYLKA 268  
134 TPNSSSAEQKOTQRFYSCLOVERIEELGAOPLRDLLEKIGNNITGPMQDNFMEYLKA 133  
269 VAGTYRATPEFTYVYISADSKSSNSNVIOVDQSLFLPSRDYVYINRTANEKYLTAAYLDYME 328  
194 VAGTYRATPEFTYVYISADSKSSNSNVIOVDQSLFLPSRDYVYINRTANEKYLTAAYLDYME 253  
329 ELGMLLGRTRTSRECOUOLELEIOUANTVPODQDRDEKTYHKMSISELQALAPMSD 368  
254 ELGMLLGRTRTSRECOUOLELEIOUANTVPODQDRDEKTYHKMSISELQALAPMSD 313  
389 WLEFLSLPLLELSDSEPVVYVGMVYLCQVSELIINTEPSIANNYLIINLVOKTSSLD 448  
314 WLEFLSLPLLELSDSEPVVYVGMVYLCQVSELIINTEPSIANNYLIINLVOKTSSLD 373  
449 RRPESAEKLELTLVYTKKSCVPRMOTCISNTDADGALGSLFVKATPDROSKIEAEGM 508  
374 RRPESAEKLELTLVYTKKSCVPRMOTCISNTDADGALGSLFVKATPDROSKIEAEGM 433  
509 ISIRIRAFERAGLVMMDEKTRQAAREKADATYDMIGFDPDILPELDDVYDGYISE 568  
434 ISIRIRAFERAGLVMMDEKTRQAAREKADATYDMIGFDPDILPELDDVYDGYISE 493  
569 DSFFQNMALYNPNSAKVMADQLRKPPSRDQMSMTPTQVNAVYVLPKNEIVFPAGIILQAPF 628

|||||  
DB 494 DSFFQNMALYNPNSAKVMADQLRKPPSRDQMSMTPTQVNAVYVLPKNEIVFPAGIILQAPF 553  
QY 629 YARNHPKALNFGSIGVYMGHELTTHAFDDQGREYDEGNNLRPMWQNESLAFNNHTACME 688  
DB 554 YARNHPKALNFGSIGVYMGHELTTHAFDDQGREYDEGNNLRPMWQNESLAFNNHTACME 613  
QY 689 QYNQYVNGERLNGRQTLGENTADNGGLKAAVNAVYKATLRKGEEOQLPAVGLTNHQLFP 748  
DB 614 QYNQYVNGERLNGRQTLGENTADNGGLKAAVNAVYKATLRKGEEOQLPAVGLTNHQLFP 673  
QY 749 VGFQVWCSVRTPRESSHEGLVTDPHSPARFVYLGTLNSRDFLRHFGCEVGSPPMNGQLC 808  
DB 674 VGFQVWCSVRTPRESSHEGLVTDPHSPARFVYLGTLNSRDFLRHFGCEVGSPPMNGQLC 733  
QY 809 EYW 811  
DB 734 EYW 736

#### RESULT 14

US-09-978-403A-526  
Sequence 526, Application US/09978403A  
Publication No. US20030050240A1

#### GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Hong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann.  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
PRIOR FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11

[illegible]



PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY VGFQKGTROLLAGRTQLEVLASLILALLLGLCVAGVQVHRPDSHSTCTTEACIRV 148  
DB VGFQKGTROLLAGRTQLEVLASLILALLLGLCVAGVQVHRPDSHSTCTTEACIRV 73  
QY AGKILSLDRGVPCEDFYQFSCGGMIRNPLPDGSRNMTFSLMDONAILKHLLENT 208  
DB AGKILSLDRGVPCEDFYQFSCGGMIRNPLPDGSRNMTFSLMDONAILKHLLENT 133  
QY TFNSSFBAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGWNITGPMQDNFMEVLYKA 268  
DB TFNSSFBAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGWNITGPMQDNFMEVLYKA 193  
QY VACTYRATPFPTYYISADSSNSNVTQVQSGFLPBRDYINRTRANEVLTAYIDYME 328  
DB VACTYRATPFPTYYISADSSNSNVTQVQSGFLPBRDYINRTRANEVLTAYIDYME 253  
QY ELGMLGGRPTSTREQOVLLELEIOLANITVPODORDEKTYHKMSISELOALAPSD 388  
DB ELGMLGGRPTSTREQOVLLELEIOLANITVPODORDEKTYHKMSISELOALAPSD 313  
QY WLEFLSLPLSLDSEPVVYVGMVYLQVSELINTEPSIINNYLIMNLVQKTTSSLD 448  
DB WLEFLSLPLSLDSEPVVYVGMVYLQVSELINTEPSIINNYLIMNLVQKTTSSLD 373  
QY RRRESAOKLELTLYGFKSCVPRWQTCISNTDAGFALGSLFVKATPDRQSKELAEGM 508  
DB RRRESAOKLELTLYGFKSCVPRWQTCISNTDAGFALGSLFVKATPDRQSKELAEGM 433  
QY ISEIRTFEBEALQOLVMDKTRQAAKADATYDMIGFDFILEPELDDVVDGYEISE 568  
DB ISEIRTFEBEALQOLVMDKTRQAAKADATYDMIGFDFILEPELDDVVDGYEISE 493  
QY DSFFQNNLNIYNFSAKVADQLRKPRPDQMSMTPTQVNAYYLPTKNEIVFPAGIIOAPF 628  
DB DSFFQNNLNIYNFSAKVADQLRKPRPDQMSMTPTQVNAYYLPTKNEIVFPAGIIOAPF 553  
QY YARNHPKALNFGGIGVMGHELTFAFDQGRREYDKENLPRWQNESLAFRHHTCME 688  
DB YARNHPKALNFGGIGVMGHELTFAFDQGRREYDKENLPRWQNESLAFRHHTCME 613  
QY QYNQYQVNGERLNGRQTLGEMINADNGILKAAVNAKKMLRKHGEEQOLPAVGLTNHQLFF 748  
DB QYNQYQVNGERLNGRQTLGEMINADNGILKAAVNAKKMLRKHGEEQOLPAVGLTNHQLFF 673  
QY VGFQVQVWCVSRTPSSHEGLVTDPHSPARFVIGTSSNSDFLHFGCPVSGPMNPQOLC 808  
DB VGFQVQVWCVSRTPSSHEGLVTDPHSPARFVIGTSSNSDFLHFGCPVSGPMNPQOLC 733  
QY 809 EVW 811  
DB 734 EVW 736

RESULT 15  
US-09-978-564A-526  
Sequence 526, Application US/09978564A  
Publication No. US20030050241A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Raoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C25  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.3%; Score 3824.5; DB 10; Length 736;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 89 VGFQKGTROLGSRQLLEVLNLAGASLLAALLGCLVALGVOYHRDPSSHSTCLTEACIRV 148  
DB 14 VGFQKGTROLGSRQLLEVLNLAGASLLAALLGCLVALGVOYHRDPSSHSTCLTEACIRV 73

QY 149 AGKILESIDRGVSPCEDFYQFCGGRIRNPLPDGRSRNNTNSLMDQOAILKHLLENT 208  
DB 74 AGKILESIDRGVSPCEDFYQFCGGRIRNPLPDGRSRNNTNSLMDQOAILKHLLENT 133

QY 209 TNNSSSEADQKQRTFLSLQYRIEELGAPLRDLIEKIGGNTTGPMDONFEVLYKA 268  
DB 134 TNNSSSEADQKQRTFLSLQYRIEELGAPLRDLIEKIGGNTTGPMDONFEVLYKA 193

QY 269 VAGTYRATPEFTVYISADSKSSNSNVIOVDGGLFSPSDYTLNRPANKXVLTAYVLYNE 328  
DB 194 VAGTYRATPEFTVYISADSKSSNSNVIOVDGGLFSPSDYTLNRPANKXVLTAYVLYNE 253

QY 329 ELGMLGGRPTSTREQMOQVLELIQLANITVPQDRDREKTIYHMSISELQALAPSM 388  
DB 254 ELGMLGGRPTSTREQMOQVLELIQLANITVPQDRDREKTIYHMSISELQALAPSM 313

QY 389 WLEFLSFLSLSEDSDEPVVYVGYDYLQOVSELLNREPSILLNLYLQVKTSSLD 448  
DB 314 WLEFLSFLSLSEDSDEPVVYVGYDYLQOVSELLNREPSILLNLYLQVKTSSLD 373

Qy	449	RRPESAOEKLLETLTGFKSCVPRMOTCI	NTDDALGFALGSLFVKATPDRQSKIAEGM	508
Db	374	RRPESAOEKLLETLTGFKSCVPRMOTCI	NTDDALGFALGSLFVKATPDRQSKIAEGM	433
Qy	509	ISEIRTAFFEBALGQLVMMDEKTRQA	AKEKADAIYDMIGFPDFLLEPKELDDVYDYEISE	568
Db	434	ISEIRTAFFEBALGQLVMMDEKTRQA	AKEKADAIYDMIGFPDFLLEPKELDDVYDYEISE	493
Qy	569	DSPFQNNMLNYPFSAKVMADOLR	KPPSRDQSMTPQTVNAYYLPTKNEIVFPAGIIOAPF	628
Db	494	DSPFQNNMLNYPFSAKVMADOLR	KPPSRDQSMTPQTVNAYYLPTKNEIVFPAGIIOAPF	553
Qy	629	YARNHPKALNFGGIGVVMGHELTHA	FDQGREYDKEGNLRPMWQNESIAAFRNHTACMEZ	688
Db	554	YARNHPKALNFGGIGVVMGHELTHA	FDQGREYDKEGNLRPMWQNESIAAFRNHTACMEZ	613
Qy	689	QYNQYQVNGERLNGRQTLGENI	ADNGGLKAYNAYKAMLRKGEBQQLPAVGLJTNHQLFF	748
Db	614	QYNQYQVNGERLNGRQTLGENI	ADNGGLKAYNAYKAMLRKGEBQQLPAVGLJTNHQLFF	673
Qy	749	VGFPAQWCVSVRTPESSHEGLVTD	BHSPARVULGTLSNSRDFLRHGCPIVGSPMNPGQLC	808
Db	674	VGFPAQWCVSVRTPESSHEGLVTD	BHSPARVULGTLSNSRDFLRHGCPIVGSPMNPGQLC	733
Qy	809	EVW	811	
Db	734	EVW	736	

Search completed: July 3, 2004, 20:15:41  
Job time : 76 secs